

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGCTCGGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCAGAGGAGA
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCAGCGGCACCGGGCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGAGCCCTGGGCTGGCCCTGCCAGGCTCGCTACGCGTGTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCTGGGGCTGTGGAGCAGCAATATGCCAGCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGCTGGTGT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC
CTGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG
CTGGACTGAGCCCTCACGCCGCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGTTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGCGCTTCTCCTTTTCTCCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCTGGCATGGGATGGGCTGGGATTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCTCTGCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGCTCAGTGGGGCTGTGCTGACCCCCAGCACAAATAAAATGAAA
CGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTATTATGCAGCTTATAATGGT
TACAAAT

6976340504

FIGURE 2

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARL PARPLGCVLSRAHGDPV
SESFVQRVYQPFLITTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGCGPQRCINTAGSYWCQW
EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTCGCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCCCACGGCGGGGACTATGGTGAAATTCCCGGCGCTCACGCCTACTCGCCCCGTGATC
CGGTTCTTGGTGCCCCCTGGGCATACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
CCGGGGCATTGTCTGTCTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTTACCGGGTCCCATGAGTGACTTCAAAAATGTGGGCTCTGGTGT
GTGAACAGCAAGAGAGACAGGACCAAGCCGTCTGTGTATGGTGTGGCAGGGGCCATCGC
TGCCGTCTTTTACACACTGATAGCTTATAGTGATTAGGATACTACATTATCAATAAACTGC
ACCATGTGACGAGTCGGTGGGGAGCAAGACGGAAGGGCCTTCTGTACTCGCCGCTTTT
CCTTTTCATGGACCAATGGCATGGACCCATGCTGGCATTCTCTTAAAAACAAATACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTGTTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGGAGCCCTGTCTCATCCGATCCTCTCCTTGTACATGGGC
GCACTTGTGCGCTGCACACACCTGTGCTGGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCCGGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTTGGGGTACATGCCATAACGGCTGGTTGACGGAAATCCGTGCTGTGTATCTCGTTTGG
ACAAGAAATAACCCAGCAACAACTGGTGAGCAGCAGCAACACAGTCACGGCAGCCACATC
AAGAAGTTACCTTCTCGTCTGCATGGCTCTGTCACTCAGCTCTGTGTTCTGTGATGTTTTGGAC
ACCAACGTTCTGTGAGAAATCTTGATAGACATCATCGAGTGGACTTTGCTTTTGCAGAAC
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCAAGTGAAGGGCGCAT
CTCACGGGTGGCTGATGACACTGAAGAAAACCTTCGCTTGGCCTGCCCGCAGCTGTGCTGG
GATCATCGTCTCATCGCCAGCCTCGTGGTCTTACCCTACCTGGGGTGTCACGGTGGGACCC
TGGCGTGGGCTCCCTCTGGCGGGCTTTGTGGGAGAATCCACATGTCGCCATCGCTGCG
TGCTATGCTTACGGGAAGCAGAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
CTCTGCCATGACAGACATGCCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAATAAGGCACGGGACGCCATGGGCACCTGCAGGGACGCTGACATGAGATGACATTC
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTGTTTGTGTAAT
GAAAGAGGCCCTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTA AAAACAAACGAAACAACTGAC
TTCATACCCCTGACCTCAGGAAACCCAAAGACACAGCTGCCCTCAGGTTGACGTTGTGTCC
TCTTCCCTGGAACTCTCTCTTGGAAACCAAAGGACTGCACTGTGCCATCGCGCTCTCGGT
CACCTGACAGCAGGCCACAGACTCTCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
TTAAACTCGGCTCTCTTTGATTGCTTCCAGTCACTAGGCCGTACAAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCACTACTCCACACATGAC
GAGGGGGGTGGCAGCTCGAGCCCGAGTCCCCGTTTACACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAATGCCCCGG
GGCAGCAAACTGACATGGTTGAATGATAGCAATTCACCTGCGTCTCTAGATCTGAGCAA
GCTGTCAGTTCTCACCCTCCCGGTATATACATAGCTAACTTTTAAATTTGACAAAAA
GGCCTATCTCAGATTTCCAGACCCCTGCCGATGACTTTTCTGAAGCTTGCTTTTCCCTCGC
CTTTCCTGAAGGTGCGATTAGAGCGAGTCACATGGAGCATCTTAACCTTTGCATTTTAGTTTT
TACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATTTCTAATGCGAGGTGCTGTAGGTAACT
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCTTCTAGTCATACTGCGGTACAGGTAA
TTGAGAAATGTACTACGTTACTTCCCTCCACACCATAGGATAAGCAAGACATTTTATAACG
ATACCAGAGTCACATGTGTGGTCTCCCTGAAATAACGCATTCGAAATCCATGCAGTGCAGTA
TATTTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTAAAAAAAATATAGACACGGTTCACT
AAATGTATTTAGTCAGAAATCTTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTCTATTTTTCG
ATTTTCAATAAAATGTCTCTAATACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSPDFKNVGLVVFVNSKRDRTKAVLCMVVAGIAAVFHTLIAYSDLGYIINKLHHVDES
GSKTRRAFLYLAAFFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCCTTLCLGYKNIHDIIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRI SRPIVNL FVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNPNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAPAE LCVVPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVLPYLGVHGATLGVGSL
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCCTTGCAGAAC
TCTGTGTGTTCCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCCAGTCACAGTGAGGGCGCAT
CTCACCGGTGGCTGATGACACTGAAGAAAACCTTCGTC



FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTGTGAGAAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAAGANTTTGNGNTGTTCCCTTTGCGGATTTTCT
CCTTTTCCAGTTCCAGTCACAGNGAGGGCGCATCTACCGGGNGGNTGATGACANTGAAG
AAACCTTTGTCTTGTCCCCAGCTNTTTGGTGCGGATCATTTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCCTACCTGGGGGTGCACGGTGCACCCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

FIGURE 7

TATTCCAGTTCGGTCACGGGGAGGGCGCATNTACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

CCCCCGCGCCCGCGCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
TGCTGCCCCGCCAGCGCAACTCCACCGTGAGCCGCGCTCATCTTCACGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCCTTCTTCTTCT
TCTTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCTCACCGTGGGTGCCCTTCTACAT
CCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGTGTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGTGGCTGGGC
AAGCCGAGGAGTGCATTCCCGTGCCTGGTACGAGGCCTCTTCTTCTTCACTCTCTCTT
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCT
GCCACGAGGGCAAGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTGCCAAGGTCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTTGCCAAACCAGCTGGGCAACGAGACAGTTGTGGCAGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGGAGCATTTGTGGGCTCATCATCTTCTCTCTGTGACCCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGTCT
GGCCTCACTGCACGTCTGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACC CGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCTCTC
TACCTGTGGACCTGTGTAGCCCCACTCTCCTGCGCAACCGGCAGCTTCAGCTTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGTCGCTGACAGCCAACT
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCTTCTAGTCGTAGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCTCCCTGT
TGCCATACTCAGCATCTCGATGAAAGGGCTCCCTTGTCTCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGAACTCCACACAGTGGGCGATCCGGCACTGAAGCCCTGGTGT
CCTGTCACGTCCCCAGGGGACCCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAAAACAGCCAGTGCGTGTA AAAAAA

0123456789

Signal sequence:

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGSIAPAFIHAKQQYIEQSQAETIYHNRFDVQSAH
RAATRGFIRYGWRWGWRVAVFTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

0002310410360

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG
GCTGGCGCCGAACC

097394-10534

Figure 1

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATTGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCATTATTCGCCGAGTTTTTGTCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAAGCGGCTCCCTACGTCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGACAGAGAATTTCAAAG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTATTATCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

FIGURE 14

GAGCCGCCGCCGCGCGCGCGCGCGCACTGCAGCCCCAGGCCCGGCCCCCCACCCACGTCT
GCGTTGTCTGCCCCGCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCTAGGGAACTT
CCGCCGAGTCGAATTTACGTGCAGCTGCCGCCAACCACAGGTTCCAAGATGCTTTGCGGGG
GCTTCGCGTGTTCGAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
CTGCTAAATTGGAATTGCTGCGTGCGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGCTGATTGGAG
CTGTAAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATCTGTTACTTGTATTTATT
GTTCAGTTTTCTGTATCTTGCCTTGTTTAGCCCTGAACCAGGAGCAACAGGTCAGCTTCT
GGAGGTGGTTGGAACAATACGGCAAGTCTCGAAATGACATCCAGAGAAATCTAAACTGCT
GTGGGTTCCGAAGTGTAAACCAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTGGCTGACCTACAGATACA
GGAACAGAAAGACCCCCGCGGAATCCTAGTGCATTCCTTGATGAGAAAACAAGGAAGAT
TTCCTTCGTATTATGATCTTGTTCACCTTTCTGTAATTTCTGTTAAGCTCCATTTGCCAGT
TTAAGGAAGGAAACATATCTGGAAGTACCTTATTGATAGTGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTTCTTCCGTTCCTGAAAAATATTTGAACTTGTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCATTGTTCGGGCACTGTCCACTGTGGCCTT
TCTTAGCATTTTTACCTGCAGAAAAAATTGATGTTACCACTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCCTAC
TGAAAAAAGAGTGGAATTTATTAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATTCCCAATTTTTTTTGGTCTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATTGTGGTTTAATTTTGACTTTTACAGGTAAGTGCAGGAGGAGTGGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTGAAGCTTAA
AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCCCAGTAGCAAAAAGATATTTG
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAAACAGCAACTT
GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTCTTTGTGTATGCATGTTTGA
ATTAAGAAAGTAATGGAAG

CGTGTCTGCCCCGCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCTAGGGAACTT

0957650

><subunit 1 of 1, 204 aa, 1 stop

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVAGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLVFIVQFSVCACALNQEQQQLLEVGMWNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIEGYAGEVLRFGVGGILFFSFTEILGVWL
TYRYRNOKDPRANPSAFL

amino acids 1-34

amino acids 47-63, 72-95 and 162-182

09/09/2017 10:50

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTATGTGTTTTCAGTTTNTGTATCTTGCCTGTGTTTAGCCNTGAACAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTC CGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTGTTGGTGCTTCGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCG

FIGURE 17

AATCCCAAATCCCCAATTTTTTTGGNCTTTT TAGGGAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

097344-0150

FIGURE 18

ATGATTATTCTGTTACTTGTTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAAATGACATCCCAGAGAAAATCCTAAACTGCTGTGGGTTCCGAAAGTTAAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

0928194151501

FIGURE 19

CAGTCCACCATGAAGCTGGGCTGTGTCTCATGGCCCTGGGCCCCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTGTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTCAGTGAACCCCTCCACCTGATTGTGTCTATGACTGGCTG
ATCCTCCAAGGTCAGCCAAAGCCAGTTTGTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGGCTTAACAGGGAATTCTCCATCACCGTGGTACAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAGAAGCTGTTTCCAGCGCCAAATTCCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGA
GGAGGCCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCTCTCCTGGTCACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATTAGAAGTAACAGTTTATCCATGATCTCACT
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGTCTGTCACATATGCATAAGTA
CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGAAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTATATCGACCAGAATGTTGTGATTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCCAACAGAAAAATAATCTGGCCCAAAATGTGAGTTGTAAGTTTGAAGAAA
CCCCAGCCTAATGAAACCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTCCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCTGTCTTTAGTTCTAGTTTGTATCCCCCATAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCAAGAGAGCTAACTCACCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTAAGAGAACCAAAACAGCTGTGCGCAAAACCCG
ACTCTGCTGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAATTCTGG
TTGTTGTAGCCTAA

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FIGURE 21

CCCACGCGTCCGCCCCACGCGTCCGCCCCACGGGTCCGCCCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCTGCTACTCTCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACTATG
ACCCCTGCAAGGCTACACCCAAAGTCTTGGTGAAGTGGCTGGTACAAACGTGGCTCAGACCCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCCAAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCACAGTGACAAC
TGGCAGCGGTTATGGCTTCAAGGTGCCCGAGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTCTCTCTCCCATCAGTTATATTGGTATAAGCAACAGACTAATAACAGGAAACCCATC
AAAGTAGCAACCCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAGCAACATCTACAGTGAAGCAGTCTCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGACCTGCCTGTCTTTGGCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATTGGCCTATATCATGCTCTGTCTGGAAGACATCCCAC
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCTCTCCATTTTGGACCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCTAAGGCCGAGGCCCTTCAAGGTGAGGACATAGCTGCCTTCCCTCTCTCAGGACACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCAGAACTCTGGGCACAACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGGCAAAAGTGTCTGTGTAATAATGCCCATTAGGC
CAGGATCTGTGACATAATTGCCTAGTCAGTCCTTGCCCTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCTGGATAGCCAAAGTGTCCGCTACCAACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGTGGAATTTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGCTTCTGGTACTCTCTCTCAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGCACAGCTATATCCAGGATCAT
TCTCTTTTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCTGGTGTCTAATAAATATCTA
ATCATAACAGC

FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416
><subunit 1 of 1, 321 aa, 1 stop
><MW: 35544, pI: 8.51, NX(S/T): 0
MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPC TYDPLQGYTQVLVKWLVRGS
DPVTIFLRDSSGDHIQQA KYQGR LHVSHKVP GDVSLQLSTLEMDDRS HYTC E V TWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGM RISLQCQARGSPPI SYI WYKQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPT TMT
YPLKATSTVKQSWDWT TDMGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYE AAR
```

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGGCGCCGCCAGCTCGCCGAGGTCCGTCGGA
 GCGCCCGCGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCCGCCCGCTCCGGGGATC
 GGGATGTCCTCTCCTCTCTCTGCTAGTTTCTCTACTATGTTGGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCATTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGTGCTCACCGGATAATGAAGGGAACCAAAA
 GTGGTGATCACTTACTCAGTCGTCTGTCTACAATACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTGCGCAGGAGATGCCTCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTTCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAACTCTAGGATT
 GACTACAACCACCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTTACTCTGGACTGTA
 CCAGTGCACAGCAGCAACGAAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAACGTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGCTTGTGAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACACCAGCATGATCCCGCAGAGCAGAGCCCTTCCAA
 ACGGTCTGAATTACAATGGACTTGACTCCACGCTTTCTAGGAGTACAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCGCCACACAACCATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTCACCGAACAGATTGAGATGAGCATTTTCTTATACAAATACCAAAACAGCAAA
 AGGATGTAAGCTGATTCTATCTGTAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCCTTTGATTACAATT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACCTATTGGATT
 ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTATTCTGACTTAAC
 TTCATTGTGCATAAGGTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATAAC
 TATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGGGATTTCCCTCAAAAT
 CAGATGCCCTTAAGGACTTTCTCTGCTAGATATTTCTGGAAGGAGAAATACAACATGTCATT
 TATCAACGCTCTTAGAAGAATCTCTTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAAATGTGAAACCAAGAAATGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGACTCCGTCTC

09978104-101501

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEEPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 25

GTCGTTCCCTTGTCTCTCGCGCCAGTCTCTCTCCCTGGTTCTCTCAGCCGCTGTGCGGAGGAGACCCCGGA
 GACGCGGGCTGCAGTCCGGCGGCTTCTCCCGGCTGGCGGCTCTGCCGCTGGGAGGTGCTGAGCGCCCTAG
 AGCTCTCCCTTGGCGGCTCCCTCTCTGCGCGGCGCAGCAGTGCATCGGGGTTGGGAGGTAGTAGGGCTCCCG
 GCCGGGAGGCGGGGTGGATCGCGGCTGGGCGAGAAGCAGCCGCGATTCCAGCTGCCCGCGCGCCCGGGG
 CCCCTCGGAGTCCCGGTTACGCCATGGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCTCTGCAAGCCGATC
 GCGCGCGAGCCACGACGACGATGATCGCGGGCTCCCTTCTCTGCTTGGATTCTTAGCACACCAACAGCTCAG
 CCAGAACAGAAAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGGCCACCGGCGAGGTGCTAACCTGT
 GACAAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTTGACCAACAGAGCTCTGCCGCTCGCGCTCTGAGCAGTTGCCCT
 GTGGGGACCTTTACCAAGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATG
 ATTGAGAAATTAATCTTGTCTGCTGCTGACTGACCGAGAATGCATTTGCCCACTTGGCATGTTTCCAGTCTAAACGT
 ACCTGTGCCCCCATACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGAGCAGAGACTGAGGATGTGGCG
 TGTAAAGCATGTGTCTCGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGGTATCAAGCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTCTC
 TCCAGCTCCACCTCACTTCCCTGGCACAGCCATCTTCCACGCGCTGAGCACATGGAACCCATGAAGTCCCT
 TCTTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCAACTCTTCTGCTCTGTAGACCAAAGTACTG
 AGTAGCATCCAGGAAGGGACAGTCCCTGACAAACACAAGCTCAGCAAGGGGGAAGAGACGTGAACAGAACCTC
 CCAAACTTTCAGGTAGTCAACCAACAGCAGCGCCCCACACACAGACATCTCTGAAGCTGTGCCGTCCATGGAG
 GCCATCTGGGGGAGAAAGTCCAGCAGCCCATCAAGGCGCCCAAGAGGGACATCTAGACAGAACTCAACAG
 CATTTTGCATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGTGTGCTTGTGGTGAATGTGGTG
 TGCAGTATCCGGAAGAGCTCAGGACTCTGAAAAAGGGGCCCGCGGAGATCCAGTGGCATTTGTGAAAGGCA
 GSGCTGAAGAAATCCATGACTCRAACCCAGAACCAGGAGAAATGGATCTACTCTGAATGGCATGGTATCGAT
 ATCTCTGAAGCTTGTAGTACGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTGTGCAATGCCAGTGAG
 AGGAGAGTTGCTGCTTTCTCCATGGGTACACAGCCGACACAGCGGGCTACCGAGCTCTCGAGCACTGGAGC
 ATCCGGGGCCCCGAGGCGAGCTCTGCCACGCTAATTAGCGCCCTCGCGCAGCACCGGAGAAACGATGTTGTGGAG
 AAGATTCTGGGGCTGATGGAAAGCACACCACGAGCTGGAAATGACAAACTAGCTCTCCGATGAGCCCCAGCGC
 CTTAGCCCCAGCCCCATCCCCAGCCCAACGCGAAACTTGAGAATTCGCGTCTCTGACGTTGAGGCTCTCCCCA
 CAGGACAAGAACCAAGGCTTCTCTGGATGAGTGGAGGCCCTTCTCCGCTGTGACTCTACATCTCAAGCGGCTCC
 TCGCGCTCAGCAGGAACGGTCTCTTTATTACCAAGAAAGAAAGGACACAGTGTGTGGCGAGGTACGCTGGAG
 CCCGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCTGAGGAGCTGCGGGTGAATGAAGAG
 ATTCCCCAGGCTGAGGACAAATAGACCGGCTATTGCAAAATTATTGGAGTCAAGAGCCAGGAGCCAGCCAGACC
 CTCTGGACTCTGTTTATAGCCATCTCTGACCTGCTGAGAACATAGGGATGACTGCATTTCTGGAATTTACTCA
 ATTTAGTGGCAGGTTGTTTTTTAATTTCTCTGTTTCTGATTITTTGTTGTTGGGGTGTGTGTGTGTTTGT
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGTGAGTCTCTTCTCCTTCTC
 TCTCTCTTTTTTTTTTAAATAACTCTCTGCGGAAGTTGGTTTATAAGCCTTGGCAGGTGTAACGTGTTGTGA
 ATACCCACCACTAAAGTTTTTAAAGTCCATATTTTCTCAITTTGCGCTCTTATGTATTTTCAAGATTATTCTG
 TGCATTTAAATTTACTTAACTTACCAATAATGCAAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAA
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAAACATCAACACTACTTTT
 AAAAACAATAATTTACTATTTTATTATTGTTTGTCTTTATAAAATTTCTTAAAGATTAAAGAAATTTAAAGA
 CCCCATGTAGTTACTGTAATGCAATCAACTTTGAGTTATCTTTTAAATATGTTCTGTATAGTTTCATATTCTAG
 CTGAAATCTGACCACACTATGCTGATGTATGGTTTCACTTGGACACCGGTGAGAAATGCTGTATTACTGTGAC
 TCTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTGCTGTAATTTAGGCTT
 GACAACCTGGGCCACCAAGAACTTGAACCTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACCTT
 GGAAGTCAAAATCAAGTGCAGTGGCGCCCTTCCATAGAGAATTTGCCAGCTTGTCTTAAAGAGTCTCTGTT
 TTTTATATACATATAATCAATAGGTCCAATCTGCTCTCAAGGCTTGGTCTCTGGTGGGATTCCTTCAACAAAT
 ACTTTAATTTAAATATGCTGCAACTGAAGAACCTTCTGATATATTGCAATATTGCTCCCATTTTCAAAATG
 TACCTTCTAATGCTCAGTTGCCAGGTCCAAATGCAAGGTGGCGTGGACTCCCTTGTGTGGGTGGGGTTTGTGG
 GTAGTGGTGAAGCCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTGA
 AAAAAAAA

0973134.101501

[illegible]

Signal sequence:

Transmembrane domain:

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCGCTGGTGCCATCTACATTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCTCTGAAATAGTCAC
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTGGCC
TTGATGATTGAAAAAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTCAAATCATCGTCATTGGGATCATTCGATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTTCACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAAATGTTGCCTGTGCCCAA
TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGTCTGCTGGAGGGGAGTTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCCTCTGGCCACGTGGTTACCTTGCAGTGACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCCTTGCTCTCGCAG
TGGCCCTTGGCAGGCCAGCCTTCAGTTCAGGGGTACACCTGTGCGGGGGCTCTGTCTATCAC
GCCCTGTGGATCATCTACTGCTGCACACTGTGTTTATGACTTGTACCTCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCATTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCTGCCCAACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCCAGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCTGCTCTGAACCA CGCGCCGTCCTTTGATTTCCAAACAAGATCTGCAACCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACGACTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGACAC
CCGTGTCACTCCTTCTCTGGACTGGATCCACGAGCAGATGGAGAGAGACTAAAAAC**TGAA**
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCTCCTCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCCGGCACCA
GTAGCAGGCCCGAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT
GTTTTTGTTTTTTGTAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACCCAACCTAATTTTTGTATTTTTAGTAGAGAC
AGGTTTCAACATGTTGGCCAGGCTGCTCTCAAACCCTGACCTCAAATGATGTGCTGCTT
CAGCCTCCCACAGTGTGGGATTACAGGCATGGGGCCACCAGCCTAGCCTCACGCTCCTTTC
TGATCTTCTACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT
CTGGTTTCTCTCCAGGCTCTGCAAAATTCCTGACGAGATAAGCAGTATGTGACCTCAGC
TGCAAAGCCACCAACAGCCACTCAGAAAAAGACGACCCAGCCAGAAAGTGACAGAACTGCAGTC
ACTGCACGTTTTTCATCTCTAGGGACCAGAAACCAACCCACCTTTCTACTTCCAAGACTTAT
TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTAAGGCTATTTTCATGATTTCTT
TGTAGCATTTGGTGCTTTGACGTATTATTGTCTTTGATTCAAATAATATGTTTCTCTCCCT
CAATTGCTGGCGTGTCTGCTGGACTGGTGACGTGAATCAAAATCATCCACTGAAA

CGGAGGAGTCTGAGT

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVQLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGNNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR
DVGGIISPSMLCAGYLTGGVDSCQGDGSGGPLVCQERRLWKLVGATSFYGICAEVNKPGVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

03978154-104531

FIGURE 29

CCCACGCGTCCGTCCTAGTCCCGGGGCAACTCGGACAGTTTGCTCATTATTATGCAACGGTCAAGGCTGGCTTGT
 GCACGAAACGGCGCGCGCGCGCGCACGCAACACACACGCGGGGAAACTTTTTTAAAAATGAAAGGCTAGAGA
 GCTCAGCGCGCGCGCGCGCGCTCGCGAGGGCTCGGAGCTGACTCGCCAGGGCAGGAATCCCTCCGCTCGCGA
 CGCGCGGCTCCGCTCGCGCGCTCGGATGGTGAGCGCTCGCGCGCGGGCGGAGAGCTGCTGCATCGAAG
 CGCGGCGACGATGCGCGCGCGCGCTCGCGCTGTCGCCCGCGCGCGCTCGCTGCTCGCCCTGGCGGCTGCTCT
 GCTCGCCCTCGGAGCGCGCGAGGGGTGAGCTTATGGAAACGAAGGAGAGCTGATGAAGTTGTGAGTGCTCTGT
 TCGAGTGTGGGACCTCTGAGATCCAGTGAAGAGCTTCGACTCCAGAATATCCAGAAGTGTGAAATATTCGACT
 ACAACGGGAAAGCAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCTCATTTGCCAGAGTTTCAACGGAAC
 CCATATCTGCAAGACGGTACTGATGCTCCCTCGCTCGAAATTTACACGGGTCACTGTTATACCATGGACATGT
 ACGGGATATTTCTGATTCAGCATGCTCTCAGCAGCTGTTCTGTGCTCAGGGGACTTATTTGTGTTTGAATATGA
 AAGCTATGCTTAGAACCAATGAAAGTGCAACCAACAGATACAACTCTCCAGCGAAGAGCTGAAAGCGT
 CGGGGATCATGTGGATCACATCACAAACACCAAACTCGCTGCAAGAAATGTGTTTCCACCACCTCTCAGAC
 ATGGGCAAGAGGCTAAAGAGAGACCTCAAGGCACTAAGTATGTGGAGCTGGTGTGCTGGCGAGACCAAC
 AGAGTTTCAGAGGCAAGGAAAGATCTGAAAGGTTAAGCAGCGATTATAGAGATTGCTAATCAGTTGACAA
 GTTTTACAGACCATGAACATTGCGATCGTTGTTGGTAGGCGTGGAGTGTGGAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCATTCACAGCTCCATGAATTTCTGAGCTGGAGGAGATGAAGCTTCTACTCTCGCAATGCCA
 TGACATGCGCAGCTTGTGAGTGGGTTTATTTTCAAGGAGCAACCATCGCATGGCCCAATCATGAGCATGTG
 CACGGCAGAGCTTGGGGGAATGTGATGGAACATTCCCTTGAGCTGTGCTGCTCAATGGCGGTTGAGAA
 TGAGCTGGGCAACATTTCCGATGAATCATGACACATGGACAGGGGCTGTAGCTGTCCATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGTTACCATTTCCATGGTTCAGCAGTTGACAGGAGGAGCT
 GGAGCCAGCCTGAGAAAGGAATGGGGGTGTGCTGTTAACTCGCGGAAGTCAGGGAGTCTTTGGGGGCCA
 GAGTGTGGGACAGATTTGTGGAAGAGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTGT
 CTGCACTCGACCACTGTACCTGAACTCGAGCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGCATCGCT
 GAAGCTTCGAGGAACAGCGTGTGAGGACTCCAGCAACTCTCTGTGACCTCCAGAGTTTGTGACAGGGGCCAGCCC
 TCACTGCGCGCCCAATGTGTACCTGCAGATGGGCACTCATGTGAGGATGTGACGCGTATCTGTAACATGGCAT
 CTGCGCAGCTCAGCAGCAGTGTGTGACGCTCTGGGACACAGGTGCTAAACTGCCCTGGGATCTGCTTTGA
 GAGAGTAATTCTGAGGGTATCCTTATGGCAACTGTGGCAAACTCTGCAAGGTTGCTTGGCAAAATGCGAGAT
 GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGGTGCCAGCGGCGAGTCATTGGTACCAATGCCCTTTC
 CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCGGATTTCTGTGCGGGGGACCAAGTGTACTTGGCGATGA
 CATGCCGAGCCAGGGCTTGTGCTTGCAGGCAAAAGTGTGAGATGGAAATATCTGCTGAATCGTCAATGTCA
 AAATATTATGTCTTTGGGGTTACAGGTGTGCAATGCAAGTGCACGCGAGGGGTGTGCAACAAAGGAAGAA
 CTGCCACTGCGAGGCGCACTGGGCACTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACGCGGCC
 CATCCGCGAAGCAGAAAGCAAGGAGGAGCTGCAGAGTCCAACAGGAGGCGCGGCCAGGGCCAGGAGCCGCTGGG
 ATCGCAGGAGCATCGCTCTAGCTCACTGACATCATCTGAGCCCTCCCATGACATGGAGCCGTGACACAGTGT
 CTGCTGCAGAGGAGGTGACGCGTCCCAAGGCCCTCTGTGACTGGCAGCATGACTCTGTGGCTTTGCCATCGTT
 TCCATGACAAACAGACAAACAGTCTCTGGGGCTCAGGAGGGGAAGTCCAGCTTCCAGGCAGCTGTGAGAA
 CAGTGCAAGGAAGGCGAGCACTTCTGTTGAGCTTCTGTAACAAATGGAATGCTTCACTGCTGCTCTGCTGAG
 AGATGAGCAGTTTACCACTCTGGCAGGCGCCAGCCCTCGACGAAAGGAGGAGGACTCAAAAGTCTGGCCTTTT
 ACTGAGCTTCCAGCAGTGGGGGAGAGCAAGGGTGGGCCAGTGTCCCTTTCCCACTGACACCTCAGCCT
 TGGCAGCCCTGATGACTGGTCTCTGGTGCACCTTAATGCTCTGATGATGCTTTTAGCATTATATATGAAAT
 AGCAGGGTTTATGTTTAAATTTATCAGAGACCTGCCACCCATTCATCTCATCCAGCAAACTGAATGGCAA
 TGAACAAACTGGAGAAAGGTAGGAGAAAGGGCGGTGAACCTCTGGCTCTTGGCTGTGACATGCTGACCAAGC
 AGTACTCAGGTTTGGAGGTTTGCAGAAAGCAGGGAACCCACAGAGTCACCAACCTTCACTTAAACAGTAAAGA
 GTTAAAAAGTGAACCAATGTAAAGACCTTAACCTCCCGTGGCCATTACTGCATAAAATAGAGTGCAATTT
 GAAAT

03978134.104501

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWI PVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTVDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFP AKKLKSVRSGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDFK
YRPLNIRIVLVGVEVWMDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPFMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRVFVEEGEE
CDCGEPEECMNRCCNATTCTLKPDCAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPAGKPAFGICFERVNSAGDPYGN
CGKVS KSSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIP LQQGGRILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRCQCNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGGQGEFVGSQEHA STASLTLI

Signal peptide:

amino acids 1-28

0978174-10154

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCTCTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATNTCCATCCAAG

092819:0450

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTACCCTGTGTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTTAAGAAGTTAAT
GAAACCATACTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAAACCCAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA
TACCAAATATCAATAACTTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAAACAAAAAATTTGCATCACTTTTAAAGAAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTCGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTGTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAATGGGTAAGGGGATGGTGGCA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTGTT
CCTTTAACAGTATGCCGGAAGCTACTGCAGCCGAAACCAAGCCCTCCAACAGTGCCT
ACAGCCTACAGCCGCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAACCGAATCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAACAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAACTCACTTGAACCTCAGGAGGCAGAGGTTCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAGCCAAAGTGCACTGGCT
CACGCCTGTAATCCCGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTGAGGATCA
AGACCATCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

09578194-104504

FIGURE 34

GCCGCGCGAGAGCGCGCCAGCCCCGCGCGATGCCGCGCGCCAGGACGCCTCTCCCGCTGCTGGCCCGGC
 CGCGCGCCCTGACTCGCTGCTGCTGCTGCTGCGCCATGGCGCGCGCGCGCGCTGGGGCGCCCGGCCAGG
 AGGCGCGCGCGCGCGCGCGGCCCCCGCGCGAGACCGCGAGGACCGGACAGGACCCGCGACAGGAGCC
 TGTAACAGCGCGACTTTTACGCAACGGGATCAGAGCGCGCGCACTTCGTATGTTCTTCGCGCCCTGGTGCA
 GACATCGCAGCGCTGCAGCGCATCTGGAATGACCTGGGAGACAATAACACAGCATGGAAGATGCGAAAGTCT
 ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCAGGGGGTCCGAGGATACCCCACTTAA
 AGCTTTTCAAGCCAGGCCAAGAGCTGTGAAGTACACAGGGTCTCTGGGACTTCCAGACACTGGAAGAACTGGATGC
 TGCAGACACTGAAACGAGGAGCCAGTGACACAGAGCCGGAAGTGGAAACCGCCCACTGCCCGAGCTCAAGCAAG
 CGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAGGCGACCACTTTATCAAGTTCTTCGCTC
 GCTGGTGTGACTCTGCAAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTTCGGGCTTGAACACTCCGAAGTG
 TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAAGTCTGCTCCGGAACAGGTTCTGGCTATCCCACTC
 TTCTCTGGTTCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAGCGGATTTGGAGTCACTGAGGGAATACG
 TGGAGTCGACGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTACGCGCTCAGAGGCCCGGGTGCTGGCAG
 CTGAGCCCAGGCTGACAAAGGCACTGTGTTGGCACTCACTGAAATAACTTCGATGACCACTTGACAGAGGAA
 TAACTTTCATCAAGTTTATGTGCTCATGCTGTGGTCTTTGTGAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA
 AAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACCGGAATATCTGACAG
 AGTATTCGTACGAGGCTACCCACGTTATGTCTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA
 GAGACCTTGAATCTTACCGCTTTGTCTGAGCCAAAGCGAAGACGAACTTGAAGAACAGTTGGAGGTCAC
 CTCTCTCGCCAGCTCCCGCACCTGCTTTAGGAGTTCACTCCACAGAGGCCACTGGGTTCCCGATGGTGGCT
 GTTCAGAAAGCAGAACATACTACAGCGTGAGGTATCTCTTTGTGTGTGTGTTTTCAAGCCAAACACACTCTACAG
 ATTCTTTATTAAGTTAAAGTTCTCTAAGTAAATGTGTAACCTCATGTGTAAACATTTCAGCTGGCGATA
 TATCCCTTTGACCTCTCTTGATGAATTTACATGGTTTCCCTTTGAGACTAAATAGCGTTGAGGGAAATGAAA
 TTGCTGGACATTTGTGGCTCCTGAGTTGAGTGATTTGGTGAAGAAAGACATCAAGAGCATAGTTTACCTGC
 CCAGAGTTCTGGAAGGTTGGCTTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTACAGTTGACTCAATAC
 GTGTTGTGTCGTAGCATGGAGCAGATTGAAATGCAAAACCCACACTCTGGAAGATACCTTACCGGCCGTGC
 TGGAGCTCTGTGCTGTGAATACTTTCTCAGTGAGGAGGTTAGCCGTGATGAAGCAGCGTTACTCTGACCC
 GTGCTGAGTAAGAAATGCTGATGCCATAACTTTATGTGTGATACTTGTCAAACTAGTTACTGTTTCAGGGGAT
 CCTTCTGTTTCTCACGGGGTGAACATGTCTTTAGTTCCTCATGTGTAACAGAGCCAGAGCCCACTGAACCTGT
 TGGATGTCTTCTTAGAAAGGGTAGGCATGGAATAATCCACGAGGCTCAITTCAGTATCTCTATTAACCTATTGA
 AAGATTCCAGTTGTATTGTTCACCTGGGGTGAACAGACAGAGGCTTTCCAGGCCCTGGGATCCAGGGAGGC
 TCTGCAGCCCTGCTGAAAGGCCCTTAACTAGAGTTCTAGAGTTTCTGATTTCTGTTTCTCAGTAGCTCTTTTAGAGG
 CTGTCTACTTGTCTGCTTCAAGGAGGTCGACCTCTAATGTATGAAGAAATGGGATGCAATTTGATCTCAAGAC
 CAAAGACAGATGTAGTGGCTGCTCTGGCCCTGGTGTGACGGCTGTGGCAGCTGTTGATGCCAGTGCTCTCTA
 ACTCATGCTGTCTTGTGATTAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
 GATAGGTTGTTGCTCTTTACCATCGAGCTACTTCCCATATAACCACTTTGACCTCAACACTCTTCACCCACT
 CCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACGTGGTGGTAGGAATCTTAGAAACAGAGCACTTATA
 CTGTCTGTGAGGAGGAGATAACAGCAGCATCTCGAACGAGCTCTGCCTTAAAGGAATCTTTATTAATCAAG
 TATGGTTCAGAGATACTCTTTTAAAAAAACCAACCTCTAGAGAGCACAACCTGTCAAGAGCTTTGTACAG
 CACAACCTCAGCTTTTATCATCAGAGTCTTGTATTCGAAGAAATCAAAGTGTACAAATTTGTTGTTTACATAT
 GATACTTCTAAATAAATCTTTTTTTTTAA

10978199-103561

FIGURE 35

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPYTLKLFKPGQEAVKYQGPRDFQTLNWMQLTLNEEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGGKVDQYKGKRDLESREYVESQLQRTETGATETVTPSEA
PVLA AEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHFRVLSQAKDEL
```

Signal sequence:

amino acids 1-32

09978494-101534

FIGURE 36

CTTTTCTGAGGAACCA CAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAAGCTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCTGCAGGATTCGG
GGTGAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTTCGGGTGTTTCAATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCTCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAA

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEGEEG
KHGKVGMRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY
RKFBVQQLDISIARLKTSMKFVNVIAGIRETEKFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

FIGURE 37

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVVCQRTAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL
LLKLHLWPQLRWLPADLAFVAVRALCCRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRRFSSYSEAESNRAARAFRLALGWDWGPDDGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGVPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKIQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPF
SKAERGHKVR LAVGSLRPDPTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTTGEPDIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GK
LLKDVFRPGDVFNTGDLLVCDQGFRLRFHVRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTTETFK
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

09750104-04504

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCATACACACTCGCTCTC
GCTTGTCCAATCTCCTCCCGGGGGAGCCGGCGCGCTCCCACTTTGCGGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACCTCGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTTTAAACACTTCTTTTCTCTCTCTCTCGTTTGGATTGCACCGGTTTCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGCTTGGCCATCGT
CCATCTGGCTTATAAAAGTTTGTCTGAGCGCAGTCCAGAGGGCTGGCTCTGCTCGCTCCCTCG
CTGGCAGAAAGGGGTGACGCTGGGCAGCGCGCAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTGTATGT
TTCACCAATGCCCTTCTTGGATCGGGGCTGTGATCTCTCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCGCGGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC
AAGGGATTGACCTGGCGGACATCCCCCTACCAGGAGATCGCAGGGGAACACTTAAAGAACTGT
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
CATAAGAAATTTGACGAATTTTCCGAGAGCTCTGGGAATCGCAGAAAGTCACTAAATGA
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCAGGACCTCT
TCACAGAGCTCGAAAGGCTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCTCGGAAACGGATGTTTCAGCTGATAAACCCCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAAGCTCAAGCCATTGTGGAGACGTGCCCC
GGAAACTGAAGATTGAGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCGCAGAGAAGTTGCAACCGAGTTTCCAAGGTGAGCCCAACCCCAAGGTTGATCCG
TGCCCTCATGAAGATGTGTACTGCCATACTGTTCGGGGCTTCCCACTGTGAGGCCCTGCA
ACAATACTGTCTCAACGCTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTGCACACAGAG
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTCTGGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGTCTGCAAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC
CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAATGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTTACCTTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACCT
GCCTGAGATCATGAATGATGGGCTCACCAACAGATCAACAATCCGAGGTGGATGTGGACA
TCACTCGGCCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAAACGCCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGGTGTCATGGATGACGTGTGTCCCAGGAGTTTGGTTTGTTCACCA
CAGAGGCCCCCGCAGTGGATCCGACCGGAGAGAGGTGGACTCTTCTGAGCCAGCGTGGC
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTCGCACTGCAGAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAAACTGCATTTAGCTATCTGAATGGCAACTCACTCTT
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACCTTACCGTTTTCTATGAGAGAGAG
CAGTAATGCAATCTGCTCCCTTTTGTTTTCCCAAAGAGTACGGGTGCCAGACTGAAGATG
CTTCCTCTTCTCTCAGCTATCTGTGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA
ATTTTTCTGACCAGGAGATTTCTTACCTTCATTGTCTTTTATGCTGCAGAAGTAAAGGAAT
CTCACGTGTAGGGGTTTTTTTTTTCTCATTAAAAAT

00078704-707507

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ
EYTCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTTELKRYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMMQENSMQVSAKVFQCGQPKPAPALRSARSAPENFNTRFRFPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHISKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDVDCPTEFEFVTTEAPAVDPDRREVDSSAAQGRHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGACG
 CAGTTTGACGCGCTGCGCGGGTGCGCCAACTACGCAAGACCAAGCGGGCTCCGCGCGGACCGGCGCGGGGCT
 TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCCGAGTTTCTGCGGAGGT
 GGAGGGAGATCAGGAAAACGGCTTCTTCTCACTTCGCGCGCTGGTGAAGTGTGCGGGAGATTTGGCAAAACGCTAGG
 AAAGGACTGGGAAAAATAGCCCTGGGAAAAGTGAGAAAGTGATCAGGAGGCCGCTCCACTACGGCAGTTTATCTG
 TCTGATCAGAGCCAGACGCGACGCGCTCCACTTCGCAAGTTCTTTCCAGGTGTGGGACCGCAGGACAGACGCGCGA
 TCCCGCGCCCTCCGTACCAAGCACTCCAGGAGAGTCAAGCTCGCTCCCCAACAGCTCAGGCGGCTTCTGCCCACGA
 AAAGTTCTGTCCACTGTGATTCTCAATTCCTTGGTGTGGTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA
 ACTTTTTCTTTTTTTTTTCTTGGTGAAGCTGCTCAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC
 TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGAGTCCCATCCATTAAAGCACTCACTCTGGAAGATTAAAGTTGT
 CGGACATGGTGACAGCTGAGAGGAGAGGAGATTCTTGCCAGGTGGAGAGTCTTACCCTGTGTGGGTGCAT
 TGTGCGCCGCGACGCGCGCGGGCGCGTGGTTCTCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGCTCCCA
 GGGCTGTGCGGGGCATCCGCTCCGCTTCTCCACAGGCTGTGTCTGCTCTGAAAGATGCTAGCAATGGGG
 CGCTGGCAGGATTTCTGATCCTCGCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCTCTAGAAGAGGAGG
 AAGAAGGGGCTTTACTAGTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCAGCCCCATCTCA
 TTTTCATCTAGCGGATGATCAGGGATTAGAGATGGGTTACCCAGGATCTGAGATTAAACACCTACTCTTG
 ACAAGCTCGCTGCCAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTGTGCACACCACTCAGGAGTCAGT
 TTATTACTGGAAAGTATCAGATACACCCGAGCTTCAACATTCTATCATAAGACCTACCCAACCACTGTTTAC
 CTCGGAACAATGCCACCTACCTCAGAACTGAAGGAGGTGTGATATTCAACGCATATGGTCGAAAATGGCACT
 TGGGTTTTAACAGAAAAGATGCATGCCACCAGAGAGGATTGATACCTTTTTTGGTTCCTTTTGGGAAGT
 GGGATTACTATACACTACAAATGTACAGTCTGGGATGTGTGGCTATGATCTGTATGAAAACGACATGCTG
 CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAATCTTAGCTTCCATA
 ACCCCACAAAGCCTATATTTTTATATACTGCCATCAAGCTGTTCACTCACCCTGCAAGTCTCTGGCAGGTATT
 TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCA
 TCAACAAAGTACATGGCTCTAAAGACTTATGGTTTCTATAACACAGCATTATCATTTACTCTTCAGATAATG
 GTGGCCAGCCTACGCGAGGAGGAGTAACTGGCCTCTCAGAGGTAGCAAGGAACATATTTGGGAAGAGGGATCC
 GGGCTGTAGGCTTTTGTGATAGCCCACTTCTGAAAAACAGGGAAACAGTGTGTAAAGAACTTGTGCACATCACTG
 ACTGTTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
 GGGAGACCATAAAGTGAGGCTCTCGCTCACCCGAGTATGATTTTGCAATAACATTGACCCCTATACACCAAGGC
 AAAAAATGGCTCTGGGCAGCAGGCTATGGGATCTGGAAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
 GAAATTGCTTACAGGAAATCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTTACGAACTGGGACCGAACCG
 GTGGCACAATGAACGGATCACTTGTCACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCGACCCATATGA
 GAGGTGGAGCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCTACGGAGGCTCTCACTGTTCAACAAAAC
 TGCAGTGGCGGTGAGTATCCCCCAAAGACCCAGAAAGTAAACCTAGGCTCACTGAGGGGCTCTGGGACCATG
 GTATAAAGAGGAAACCAAGAAAAAGAACCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAA
 GAAGAGAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGTGGCCTAAGCGTCA
 GGCTTGTCTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAACCTGTCTGCTCAGTG
 CCAAGGTCTACTCTTGCAGGCCACACTTAGAGAGAGTGAGATGTTTATTTCTCTCGCTCCTTTAGAAAAACGTG
 GTGAGTCTGAGTTCCACTGCTGTGCTTCACTCACTGACCAAAACACTGCTTTGAATTATAGGAGAGAGAACATA
 ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACCTACCTTTGATAAATTAC

CG97B104.F01501

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEGALLAQA
GEKLEPSTTTSQPHLIFILADDQGFRDVGYHGSEIKTPTLCLKAAEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC
MPTRRGFDFTFFGSLGLSGDYIYTHYKCDSPGMCGYDLIENDNAAWDYDNGIYSTQMYTQVRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNIIIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMSGTGLQSSQSPSECSTGNCLQEILATATGSPLSLSATWDRGTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCCTCTGCCCTTGGAGCCTTGCCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTCGGGAACGCGGCCAGTGC AAGGCATCACGGGTGTTTAGCATCGGCACGTGAGCCT
GGGGTCTGTCACTATGGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAAGTGCCTGGGACCAAAACAAAT
GCAGATGCTTTCCAGGATACACCGGGAACCTGCAGTCAAGATGTAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCCTTTTGCCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTCTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAAATGTCACA
TTGGTTTCGAACGTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAGGCAAAAAATAAAAATGTTACCCGAGAACCACCAGGACTCC
TACCCCTAAGGTGAACCTTGACGCCCTTCAACTATGAAGAGATAGTTTCCGAGGGCGGGAAC
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTAAATATCTCGGTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAACAGGATAGAGAAGATGATTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCGGCCTTGGCAGGTACAAAGAAAGACATTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTGTTGTGAAAAACAGTAAACATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAAGTGTATCAAGGAACATGATGC
TACCAAAAGCATCATTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAATCGCAGTGG
ATGGCGTCTTGCTTGTTCAGGCTTATGTCCAGATAGCCTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTGACTTTGTATGTCACTTCCCTGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCCTTCTTGATAAAGATATGCCAATATTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTCTGAATCTTTCCNCATTATATATAAAATNTGGAAANGTCAGTTTATCTC
CCCTCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCAACACATTCTA
GAAAAATAGAAAAAAGCAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGGA
AACTATGACATCAAAGATAGACTTTTGCTTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

007347.101501

FIGURE 45

MPLPWSLALPLLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPPK
VNLQPFNYEEIVSRGGNSHGKKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCTTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC
AGAATGGGAGCTGACTGATATGCTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTAAAAGAAAAAGATATACT
TGTTTTGCCCTTGACCTGACCGACACTGGTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAAATGTCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCACAAGATGACAACCAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTGGATCTCAGAACAACTTCTTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTATTTTAAATC
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

0997613410594

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLEENGLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG
 TTGCATCTTCTACACACTACAGCTATTTGTTAGGTTGCCTGCGGACACGCTGGGCCCTCTGTCC
 TGATGCTGCTGAGCTCCTCTGGTGTCTCTCGCTGGTTCGTCTACCTGGGCTGGATCCTGTTTC
 TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGCTGAGCCTGAT
 GTGGCTCAGTTTCCGGAAGGTCGAAGAACCCAGGGCAGGCTAAGAGGCACTGAGCCTCA
 ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCTGTG
 GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
 CTGGGTCCTCACTGTGCCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
 CAGTGGTCTCGGTTCTCTGCGAGCGTGAGGGAAGTCTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
 GCTGCCCTGCAGTTGCCAGGGCCTATAACCACCTACAGCCAGGGCTCAGACCTGGGCCCTGCT
 GCAGCTCGCCCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCCCATCGCTTCC
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
 CTACGCAATCTGCGCCTGCGCTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAGCT
 GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCAGCCTG
 GGGTGAGAGGCCCTCTGTCAGGGAGATTCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACCGA
 CACTGGGTTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT
 GCTGCTGACCAACACAGCTGCTCAGAGTTCTCTGGCTCGAGGCTCGAGTTCAGGGGGCAGCTT
 TCCTGGCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
 TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCATGGCCCTGGGAGGCCAGGCT
 GATGCACAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG
 CTGCCCACTGCTTCAATTGGGCGCCAGGCCCCAGAGGAATGAGCGCTAGGGCTGGGGACCAGA
 CCGGAGGAGTGGGGCCTGAAGCAGCTCATCTGTCATGGAGGCTACACCCACCCCTGAGGGGGG
 CTACGACATGGCCCTCCTGCTGCTGGCCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCG
 TCTGCTTGCCTATCCTGACCACCACCTGCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
 GCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCTCTCTGGGGCCTAG
 GGCCTGCAGCGCGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
 TGTGTACCAGTGTCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGGTG
 CATGAGGTGAGGGGCACATGGTTCTTGCCCGGGCTGCACAGCTTCGGAGATGCTTGC AAGG
 CCCC GCCAGGCCGGCGGTCTTACCGCGCTCCTGCGCTATGAGGACTGGGTGACAGTTTTGG
 ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCGAGGCTGAGCCTGGAAGCTGCTTGGCC
 AACATAAGCCAACCAACCAGCTGCTGAGCAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
 AGGCAGGCCAAATGGCATTACTGCCCTGTCTCCCCACCTGTGTCATGTGTGATTCAGGCAC
 CAGGCAGGCCCCAGGAAGCCACAGCAGCTGTGGGAAGGAACCTGCTTGGGGCCACAGGTGCCCA
 CTCCCCACCTGTGAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC
 AGGCGTCTCAGCTTTCCTCCTCTTACTCTTTCAGATACAATCAGCCAGCCACGTTGTTT
 TGAAAATTTCTTTTGGGGGGCAGCAGTTTTCTTTTAACTTAAATAAATGTTAC
 AAAAAAAA

CGGTGTCATTTCTG

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSCGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAULTAAHCFIGRQAPPEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLDPDGERG
WVLGRARPAGAGISSLQTVPVTLTGPRACSRHAAPGGDGSPIIPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

03978394-04604

2000

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><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
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MLRRRGSPGMGVHVGAAALGALWFLCTGALEVQVPEDPVVALVGTDATLCCSFSPSPGFSLAQ
LNLILQLTDTTKQLVHVSFAEGDQDGSAVANRTALFPDLLAQGNASRLRLQVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDQGQVPL
TGNVTTQSMANEQGLFDVHSLVRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTPFPEA
LWTVTGLSVCLIALLVALFAVFCWRKIKQSCEENAGAEDQDGEQSGKTALQPLKHSKDED
DGEIA

Signal peptide:

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCTGTGACCCCTTGAGAAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGTGCTTTTGTAGGGACTTCTTTCCCTTGCTTCTCAGCAACATGAGGCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAATAATGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTTAGAAAAGGACGGCTCCTTATTCTACTCCACTC
ACAAACATAACAAATGGTTCAGCCCACTTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAAAGCTCATCATTCCTCCTCTGC
TCTGGGCTATGGAAGAAAGGAAAAGGTAATAATTCCTCCAGAAAAGTACACTGATATTTAAATA
TTGATCTCCTGGAGATTGCAAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAACCTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTTCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCCTTTTAAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTCTTCTTGCTTTGTTTTTATTTTTATATATTTTTT
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAAGACTTCTGGACAATTTTTCATCTTTCACAG
ATATGAAGCTTTGTTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAAGGTTATAGCACAAATTAGCACCCATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAACTGGCTCTGAGTCTCTGCTTGAGGACCAAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCCTGTAATCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTTCGAGACCAAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCGTGAATCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCGAGGTTGCGGTAAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACCGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGTAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACATAACAATAACA
TTGTATCATAAGATAAAGTAGTAAACCACTCATATTTCCCACTTCTGCTCATCAAAAA
TGAAGTTAGCTGGGTGTGGTGGCTCATGCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG
TGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCAACCTGTAGTCCAGCTACTCGGGAG
GCTGAGACAGGAGATTGCTTGAACCCGGGAGGCGGAGGTTGCACTGAGCCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATT

FIGURE 53

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRTKGGDMLLVHYEGYLEKDGSL
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKFEFKHGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL
```

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCACCCGA
CTAACATCTCAGTCTCTGAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC
CTGCCACCCCTCAACGCTCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTACAACTGCTACATCATGAACCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATTGTGGGTGCCCTCCGTCGGGGGCTTCTCGCTGTGGTTCATCTTGGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCAAGTAGTGGGTGGCCGGCC
CTGCAACCTCCCGTGTCCCGTCTCCTCCCTCTCCGCTGTACAGTGACCTGCTGCTCG
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCTCCTGAACCCCG
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGGCTTGGGGAGAGGAGAGAAAGGCTCCCAACCTGCCAGTCCCTGG
GGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCGCTGTCACTGCCAGTGCTTGCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTCTGTGCTGACAGCGCTCCCTCAGGAGGGCTTGGCCTGGCAGCGCTG
TGCTCTCCCTGCTCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGA
AACTTGGAGGGGCATGTTAAGGGATGACTGTGCATTCAGGGCACTGACGAAAGCCAGGG
CTGCAGGCAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTCCCAAGCGGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG
GCTCTGCCTCTCCATGGGTAAACCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGGAAGGGAAGCCCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG
CTACTCGTCTCTCCCAACAACCTCCCTTGTGGGGAACAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTCACGCCGTGTAATCCAGCACTTTGGGAGGCCAAGCGGGTGGATTACCTCCAT
CTGTTTGTAGAAATGGGCAAAACCCATCTCTACTAAAATAACAAGAATTAGCTGGGCGTG
GTGGCGTGTGCTGTAATGCCAGTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
GGAAGCAGAGGTTGCAGTGAACAGATAGTGATAGTGCCACTGCAAATTCAGCCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAAA

CG578194-101504

0906

<subunit 1 of 1, 215 aa, 1 stop

MHRDAWLPRPAFSLTGLSLFSLVPPGRSMETVTPATNLVNLGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLNVQPEDEGI
YNCYIMNPPDRHRHGKGIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPPDGAK

Signal peptide:

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 56

GTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAAGTGGACTTACCAGGAGTGCAACAAGTCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAAGTCTACATCATGAACCCCC

007044-1050

FIGURE 57

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNACATA
CCTGCCACCCCTCAACGTCTCAATGGCTTTGACGCCCGCCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGC
TGAGAAACGTGCACCGGAGGATGAGGGGATTTACAAC TGCTACATCATGAACCCCC

3378194-30759

FIGURE 58

TGCGGCGACCGTTCGTACACCATGGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCCTCCTGT
TCCCTTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGGAGCTACACCCCCAGTGGTGTGCTGCTC
CTGGTGTATTTGGGTAAACCACTGGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACTCTGCTCCAGAAGA
CCGAAGAGCTACTTCACTGAATCTGGCTGAACCTGGAACTGCTGCTGCTCATCTATTGACTGCTGGATTGACAAATA
TCAGGCTGGTTTACAACAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGCTCCCTGGCTTTG
GGAAAGACCTTCTCATCTGGAGTTCTGGAGCCCAAGCAAAAGCAGCGTGGGTTCTATTCCACACCATGGTGGAGA
GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCAGGCCCAAAATG
AAAAACGGGCCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAAGCTGTATGGGGGCCCCCTGGTGC
TGGTTGCCCCAGATATGGGCAACATGTACACGCTCTACTTTCTGACGCGGAGCCGAGGCTGGGAAGGACCAAGT
ATATCCGGGCCCTCTGCTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAAGACCTCGCGGCTCTGGCTTACAGGAG
ACAACAACCGGATCCCACTCATCGGGCCCTGAAGATCCGGGAGCAGCAGCGGTGAGCTGCTCCACAGCTGGC
TGCTGCCCTACAACATACACATGGTCACCTGAGAAGTGTTCGTGCAGACACCCACAATCAACTACACACTGGCGG
ACTACCGCAAGTTCTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGCGAGGACACAGAAGGCTGGTGG
AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCTCTATGTAAGTGGCGCTCCCAACACAGACTCCCTTACT
ATGAGAGCTTCCCTGACCGTGACCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTTGAAGAGTGGCC
TGCAAGTGGCAGGCTGGCAGAGCCGACAGGAGCACAAGTGTGCTGAGGAGCTGCCAGGACGAGCAGCATCG
AGATGTGGCCCAACGCCACACCCCTGGCCCTACTGAAACGTGTGCTCCTTGGGGCCCTGAATCCTGTGGCCACAGGA
CTCCTGTGGCTGGCCGTGGACCTGCTGTGGCCCTCTGGGCTGTGATGGCCCAACCGCTTTTGAAGATTGTGA
CTACCAATTCAGAGCCCGCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGCTTTGTTATCCTTTCTCT
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGA
ACTGCTGTGACTCTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCAGTCCCTGGCTGGGGCCATG
TGTCCCCCTATTCTCTGGGGCTTTTCATACTTGGCTACTGGGCCCTGGCCCGCAGCCCTTCTATGAGGATGTT
ACTGGGCTGTGGTCTGTATCCAGAGGTCCTCAGGGATCGGCTCTTGGCCCCCGGGTGAACCTTCCACACACCA
GCCACAGATAGGCTGCCACTGGTCTGGGTAGCTAGAGTGTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
TGACTGGCTTCTTGGGCGAGCTAGTAGCTCTGTCAGGACAGGGGCAATTTGTTCGCTTCTGCTGGTTCCAGGCG
CCTGGGACATCTCACTCACTCCTACCTCCCTTACACACAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG
CCCCAGTCCCGAGGCTGTGTTCCAGGGGCCCTGATTTCCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC
CTCCCTTACCCCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTTGAGCCATGGCCCTCTGGGAACCTATGGA
GAAAGGGAATCCAAGGAAGCAGCAAGGCTGCTCGACGCTTCCCTGAGCTGCACCTCTTGCTAACCCCAACATCA
CACTGCCACCCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCAGAGGCTGAGGATGGGGCTCCTATCCAC
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCAGAACTTGAATGGGACCTGAGAGAGCAGGGGTCCCC
TGAGGCCCCCTAGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCTGTGGCAGCAGGCAAGGAGT
CAGGGCTGCCCTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCAGAAAAAGGTACAGCCTCTAGGT
GGGTTTCCAAAGACGCCCTTCAAGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGACGCTGGATTTTCTCTG
TTGCATACGCTGGCTGACTGTCTCCCTTGTCTCTGAGTGGCCCAATGGGGCTCTGAGCAGGCTGTATCTG
GATTCTGGCAATAAAGTACTCTGGATGCTGTAAAAA

097814.101501

FIGURE 59

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGDVDRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSVAVSTSWLLPYNYSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWL
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLGPG
```

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGACGCGCGACATGGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCTGACGACGCGCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTCTCTCGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTC AACCGCAACGAGGAT
GCCTGCCGTATGGCAGTGCCATCGGGGTGCTGGCCTTCTGCGCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCTGTGGTTTGTGGTTTCTGCTTCCCTACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACCTGCCA
GCCCCCTCTCTTTCACCTGTTCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGCTGGCAGAGCCACCCCCAAGTGCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCTC
CAGCTTCCCCCGGCCGGGTGAGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAAGGCTCTGTGTCTCTCA
CTCAGGTTTGCTTCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCTGTGCCGCT
GGCTCTCGGGCTGCTCCCGTGGTGTGAGGGCGGGCTGGTGTCTATGGCACTTCTCTCTTG
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCATGGCTCCAGACTCTGTCT
TGTGCCGAGTGATTATAAAATCGTGGGGAGATGCCCGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDILLFSALWTFWLVGFC
FLTNQWAVINPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FIGURE 62

GAGCCACCTACCTGCTCGAGGCCAGGCTGCAGGGCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCCFTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGGACGAGGTGATGCGAGGAAGCGGAGCCAGAGGGG
 ATGTTCAAGGCTTCAGGAGCTCAAGAGAAAAGCCCGGGGCTACTCCGCTGGTGGCCCCCTGTTTGTGCTGCTG
 GCCCTAGTCTGTGCTGGCTTCGCGGGGGGTGCTACTCTGGTATTCTCTAGGGTACAAGGCGAGGTGATGGTCAGC
 CAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCGGGGAATCTAGTGCC
 TCCGCAAGTAAACCGCCAAAGCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCTGGGAATCTACTAC
 AACTCCAGCTCCGTATTCTCTTTGGGAGGGACCCCTCACCTGCTTCTCTGGTTCATTCTCCAATCCCCGAG
 CACCGCCGAGTGTGCTGAGCCCCGAGGTGGTGACGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC
 TCGGCTGCGCTCCCTACAGGGCCGAGTACGAAGTGAACCCGAGGGCTAGTGATCTCTGAGAGCCAGTGTGAAA
 GACATAGCTGCATTGAATTCAACCTGGTGTGTTACCGCTACAGCTAGCTGGGCCAGGGCCAGGTCTCCGGCTG
 AAGGGGCTGACCACCTGGCCCTCCAGCTGCTGTGGCACTGCGAGGCCCCAAGGACCTCATGCTCAAACCTCCG
 CTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCTGGAGAAAGAGCTC
 ATCACCTCGGTGTACGGCTGCAGCCGCGAGGAGCCCGTGGTGGAGGTTCTGGCGTCCGGGGCATCATGGCGGT
 GTCTGGAAGAAGGGCTGCACAGCTACTACGACCCCTTCTGCTCTCTCCGTGACGCGGTGCTTTCCAGGCTGT
 GAAGTGAACCTGACGCTGGACAAAGGCTGCACTCCAGGGCTCTCTCAGCACCCCTGACTTCCCCGACTACTAC
 TCGCCCCAAACCACTGCTCTCGCACTTCAAGGCTGCTCTCTGGAATACGCTTGGCCCTCTGGTTTGAATGCC
 TATGCACTGAGGAGGCGAGAAGTATGATTGCGCGTGCAACCGGCGATCGAGAACAGGAGGCTGTGT
 GGCTTGGCGATCTCGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCAGGCGGGATCACCATCAACTTCACC
 TCCAGATCTCCCTCACCGGGCCCGGTGTGGCGGTGCACTATGGCTTGACAACAGTCGGACCCCTGCCCTGGA
 GAGTTCCTCTGTTCTGTGAATGSACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCACCGGCTGGAT
 GAGAGAACTGCGTTTCAGAGCCCAATTCCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCAAGGCTCTGT
 GATGGCGACCTGATTGCTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCAACC
 TTCAGTGTGAGGAGCGAGGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCGACTGCAGGGAACGCG
 TCCGATGAGGAGCACTGTGACTGTGGCTCCAGGGCCCTCCAGCCGATTTGTTGTGGAGCTGTGTCTCCGAG
 GGTGAGTGGCCATGCGAGGCCAGCTCCAGGTTCCGGGTGCACATCTGTGGGGGGCCCTCATGCTGACCCGAC
 TGGGTGATAACAGCTGCCACTGCTTCCAGGAGGACAGCATGGCTCCAGCGTCTGTGGAACCGTGTCTCTGGGC
 AAGGTGTGGCAGAACTCGGCTGGCTCGGAGAGGTGCTTCAAGGTGAGCGCGCTGCTCTGCAACCCGTAACAC
 GAAGAGGACAGCCATGATACGACGTGGCGCTGCTGCAGCTCGACACCCCGTGGTGGCTCGGCCCGCTGCGC
 CCGCTGTGCTGCCCGCGGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCTGGGGCGGCTTG
 CCGAGGGCGGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGAGTTGATCCACAGGACTGTGCGACGAG
 GCCTATGCTACAGGTGACGCCACGCTGCTGTGCGCGCTACCGCAAGGGCAGAAGGATGCTGTGAGGT
 GACTCAGGTGTCCGCTGTGTGCAAGGCACTCAGTGGCGCTGGTTCCTGGCGGGCTGGTCACTGGGGCTG
 GGCTGTGGCGGGCTTAACCTACTTCGGCTCTACACCCGCACTACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG
 ACCTGAAGAACTGCCCTCTGCAAGCAGGGCCACCTCTGGACTCAGAGAGCCAGGGCACTGCCAAGCAGG
 GGGACAAGTATTCTGGCGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGTGGCACTTGTCTGTGCTC
 CTGATGTCTGCTCCAGTGTGCGAGGAGGATGGAGAAGTGCCAGCAGTGGGGCTCCAGACGCTCCCTTAAGCAG
 CAGGCCACACCGCCCTTCTGCTCCCAATTCTCTCTCCGTCCCTCTCAAGCTGCTGATCTGGATCTGGAACT
 GCAGTGGCTCAGCAGCAAGATGTGGTTTACATCTCCGAGGAGTGTCTGAGTGGCGGCCCATCTGTACAGAGG
 CTGTTTGGGAGCTTGCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGTGCTTAACTTGGATCTGGGAAT
 GGAAGTGTGCTCCATCGAGGGGACCTCAGAGCCCTGGAGACTGCCAGTGGGCTCTGTGCACTGTAAAGCZAA
 AAGGTTGGGGAAGTCTGACTCCAGGGTCTTGGCCCAACCCCTGCTGCTGCTGGCCCTCAGCGCCCAAGCCCT
 CACTGGGAGGTGAGCTCAGCTGCCCTTTGGAAATAAGCTGCTGTATCAAAAAAAAAAAAAAAAAAAAA

09978194-101501

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQDGGDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YNNSSSVYSFGEGLPTCFFWFILQIPEHRRMLMLSPVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLRLKGPDLASSCLWHLQGPKDMLML
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSPTYFSPSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTCQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFCLSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDDGQPDCLNGSDEEQCEQGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD
CGLQGPFSSRIVGAVSSEGEVWPQASLQVRGRHICGGALIADRWVITAAHCFQEDSMASTVL
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSAYRYQVTPRMLCAGYRKG
KKDACQGDGGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

[illegible]

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCG
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCAGAT
CTCCCTCACGGGCCCGGTGTGCGGGTGCCTATGGCTTGTACAACAGTCGGACCCCTGCC
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAAAACTCGCTTTGCAGAGCCACATTCCAGTGCAAAGAGGA
CAGCATATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGCACTGTGATGGGCGGCCGACTGCAGGGACGGCTCGGA
TGAGGAGCAGCTGTGACTGTGGCCTCAGGGGCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CTCCGCAAGGTGAGTGGCCATGGCAGGCCAGCCTCAGGTTCCGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTAGCCGCTGGGTGATAACAGCTGCCCACTCTCCAGGAGGACGACAT
GGCCTCCACGGTGCTGTGGACCGTGTTCTGGGGCAAGGTGTGGCAGAACTCGCGCTGGCCCTG
GAGAGGTGTCCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCGAGCTCGACCACCCGGTGGTGCCTCGGCCGCGCTGCGCCC
CGTCTGCTGCTCCCGCGCGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCCTGTGAGGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGTTTCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCG
CCTAACTACTTCCGCGCTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GTGACTGAGGAAGTGCCTCCCTCGTCAAGAGAGGGCCCACTCTGGACTCAGAGAGCCAGGGC
AAGTCCCAAGCAGGGGACAGATAT

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCGCGCG
AGAGAAGGGTCTTACC GGCCGGGATTGCTGGAAAACCAAGAGGTGGTTTGTGTTTTTAA
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACTCTCCGACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTGCGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTCATCATTACGGAT
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCGGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGGATGTCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCAAGAGGTGGTAAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTGTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCTTCCAGTGCACT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAAATCGTTGCAAAATCAGATTACACTGTGCATGTCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646
><subunit 1 of 1, 354 aa, 1 stop
><MW: 39362, pI: 8.35, NX(S/T): 2
MSNSVPLLCFWSLCYCF AAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLR TSKDPEHE
GCYLSVGHSQPLEDCS FNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL
PLAHQLYTD AVNNTRVVGH SIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGT V
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYN AKMRNKRNSKMYLKTRAGMFFRGNLQSL ECP
```

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGAGCGCTGGGCGGACGCTGGGCTGGGCAAGGCGGGGCGCCGGGCGAGCCACCTCTTCCCCCTCCCCCG
 TTCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGCGGGCTGGGGGCTGACAGT
 CGGCAAAAGTTGGCCCCAAGGAGGAGTGGTCTCAAACCCCGGCGAGTGGCGACCGAGCCAGCAGGGGCGCTCG
 TCGCTTCGGGCGGGCTGTAGGCGAGGGCGCGCCCGAGTGCAGACCCGGGGCTTCAGGAGCGCGCCCGGAG
 AGAAGAGTGGCGGCGGACGGAGAAAACTCCAAAGTTGGCGAAAGGCAACGCCCTACTCCGGGCTGCCG
 CGGCTCCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCGCTGGGAGGGCG
 CACAGGGAGGCTGGGCGCCCGGGGCTCCGCGCGACCCCATCGGGTAGACACAGAAGCTCGGGACCCCTCCG
 GGCTTCGGACAGCCAGAGTGTGTTGGCCACCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCATCCAG
 ACCGGATTATTTTCCAAATCATGCTGTGAGGACCCCGCAGTGTCTTTAGAAAGTGCAGGGCACCTTACAGA
 GCGCCCTGTGTCGGGACAGCCGCACTCCCTGCCAACTGCACCTGGCTCATCTGGGCAAGGAACAGACTG
 TCACCATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCGCTTAACCTACGCTCCCTCTCCAGCAC
 TGATCTCCCTGTGTGAGGCGACCTCCGACCCCTTGCAGCTGCCGGGGCAACGTACCATCACTTACAGCTATG
 CTGGGGCGAGACCCATGGGCGAGGGCTTCTGTCTCTCTACAGCCAAAGATTGGCTGATGTGCTCAGGAAG
 GAGATGCAGTGCATGTATGACGCGCTGGGCGCTGTGATCTGCTGCCAGCGCTGTGATGGGGTTGATGCTTGGGAGTGGCT
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTCCCTGGCTGACCCCAAGACCGCTCCCTCCCTGCTGCTGCAATG
 TCACCTTGGAGGACTTCTATGGGTTCTTCTCCTCTCCTGGATATACACACTAGCCCTCAGTCTCCACCCCGAGT
 CCTGCCATTGGCTGCTGGACCCCATGATGGCGGGGCTGGCGCTGCGCTTACAGCCCTGGACTTGGGCTTTG
 GAGATGCAGTGCATGTATGACGCGCTGGGCGCTGGGCGCTGAGAGCTCCGACTACTGCTAGTCTCAGCCACTTCA
 GCAATGGCAAGCTGTCACTGTGCGAGACACTGTCTGGCCAGGCTGTTGTGCTACCCACAGATTGCTTGGAGCA
 ATGGTCTGGGCTTCAATGCCACTTCCATGTGCGGGCTATTGCTTGCCTGGGACAGAGCCCTGTGGCTTAGGCT
 CTGGCTGGGAGCTGCGGAAGGCTTAGGTGAGCGCTGTACAGTGAGGCAAGCGCTGTGACGGCTCATGGGACT
 CTGTGACGCGCAGAGTAGGAGGAGCTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGTGGCACCT
 CTGCTGCCAGCGCTGTACTGCTGTGACGCTGCACTACCAAGACTTCTGTGCTGATGGAGCAGATGAGA
 ATGGGCGAGCAGATGTGCGGCGCGAGTGATGAGTGGGACTGCTCTATGTTGCCCGCAAGGTCATTACAG
 CTGCACTTATGGCAGCTAGTGTGCGGCGCTGCTCCTGGTCTGCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
 CAGGACCAACCCGGAGCCCTTGGCCCCCTCTCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCCACCCC
 CTTCTTACGGGCGCTCATTGCCAGGGTGCCATCCCACTGTAGAAGACTTTCCTACAGAGAACTCCTAATGATA
 ACTCAGTGTGGGCAACCTTGGCTTCTCTGCTACAGATCTTACGCCAGGATATGATCCAGGAGGTGGCCAGGTG
 CCGCGCTGTGTGAGCGGGCGCTTGTGTCGACGCTGTTACGCGCTCTCCGCGCTGGGGCTTGTCTCCCTGAA
 CCAACACCCCGGCTCGGGCTCTGAGGCGAGATCCAGGTCAACCTTCTGCTGCTCCCTTGGAGGCCATAGATG
 GTGGCACAGGTTCCAGCCCGTGAAGGGCGGGCAGTGGGTGGCAAGATGGGAGCAGGCACCCCACTGGCCATCA
 AGGCTCCCTCCCATCTGTAGCACGTCTCAGCCCCCACTACTGTCTGCTGAAGCCCCAGGGCCACTGGCTTCA
 TGGCCCTAGAGCCATCACTATTGTCTGGAGTGGTGAGGCGCTGCGAGCGCGCTGTTGCCAGCCTGGGGCCCC
 CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACAGTGTGCTACTGG
 TGGCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGG
 CTTACTGAGGCTCCTCCCTGGGGGCTTACTCATAGTGGCACAACTTTTAGAGTGGGCTGAGCTCCCTCCCTCC
 ACCACTTCTCTCCTGTCTGGATTTCAGGACTTGGTGGGCTCCCGTTGACCCATGTAGTGTCTATAAAGT
 TAAGTGTCTCAGGCAGGGAGGGGCTCAGAGTGTCTCTGTACGTGGCTGACGCGAGACACCCGAGTCCCT
 TCACCAACCTGTCTCCCAAGCCACCACTTTGGGTGGCTGTTTTAAAAAGTAAAGTCTTTAGAGGATCATAG
 GGTCTGGACACTCCTTGGCAACCTTACCCAAAGTGGCTTAAGCACCAGGAATGCCAATGCAATAGAGA
 CCTTCAGCCCCCAAGGGGAGGATTGGGCAGAACCTGAGGTTTTGGCCATCCCAATCCCTCTTACAGGGCTGG
 CTTCAAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGCATTGCTCAGTAAGTTGAGTCAAAAATAA
 GGAATCATACATCTC

09978194-101501

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSLQLPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MQGGFLLSYSQDWLMCLQEETFQCLNHRCSVSAVQRCDGVDACDGDGSEAGCSSDPFPGLTFRP
VPSLPCNVLTLEDYGVFSSPGYTHLASVSHPOQSCHWLLDPHDGRRLAVRFTALDLGFGDAVH
VYDGPFPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGNATYHVRGYCLP
WDRPCGLGSLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCDKCYETWVCDGQPD CADGSDEWDCS
YVLPKRVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFPPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRIMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPT TVEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPFGPTRSPFPGPHTAV
LALAEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCTGAACCATATATTGTTATCACTGGATTGGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTGGCACTGATACCAG
AAACCAACATTTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAAGAAGTTTTGTAAATTTTATATTACTTTTGTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL
```

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGINTTGCCGAC

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCTGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCCGCGTGGGCATGGGCGCACTGGCCCCGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGTCTCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCCACCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCGCAGCGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCCGCCAATTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCCGCACTCCTACATAGACAGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGAAGACCTCGTACCATCCCCAAAGGCTCAATACTTCTTTTCTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTCTTTTTGCGCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGTTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTG
AAATTGGAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTATGTCGGTGGTGG
AAGCTGTGGCCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTTCGAAACACCTTGCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTACGC
CCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTATCTTCGACAGAGCCCAGAA
GAGGTGGGCTTCGACGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCTCCTTGTCTT
AATCGTCTGTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCTGCA
ATGATGAGTCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTCTCTCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTACAC
TGTCTTTTGATTCTTGATTITCAAGCTTCAAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAACTTCATTCTAA

CGCTGCTGGCCAGTGGTCTCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG

[illegible]

```
><subunit 1 of 1, 518 aa, 1 stop
```

MGALARALLPLLAQWLLRAAPELAPAFPTLPLRVAAATNRVVAPTGPFGTPAERHADGLAL
ALEPALASPAGAAFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFVDVTVKYTGSGWTFGVGEDLVTPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGALGPVAGSGTNGGS
LVLGGEPSLYKGDIIWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISIIYLRDENSRSFR
ITILPQVYIQPMMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIGAABVSEISGFFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVILVLLLPFR
ORPRDPEVUNDSSILVHRWK

Signal peptide:

Transmembrane domain:

amino acids 466-494

amino acids 170-173 and 366-369

amino acids 10-31 and 197-118

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTTGGCGGGCATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGAGGC CGCGGC
GGC**ATG**GAGGCGCTGCTGTCTGGGCGCGGGGTGTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCGTCGCGCGGCATGGGCAACCTGCGGGGCCGACGCGCGTGG
TCACGGGCGCCAAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGTCTGGCCTGCGCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCACTTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCCTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGACCCGTGAGGCGTTTAACTTGTCTGCTTCGGGTGAACCATAT
CGGTCCCTTCTGCTGACACATCTGCTGTGCTGCTGAGGCGTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCCACTGTGCGGGACGTCTTGACTTCAAACGCTTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCACC
CAGGGCCTGTAACTCGGAGCTGTTCTTGCGCCATGTTCTTGGATGGCTGCGCCACTTTTGG
CGCCATTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCACAGACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTGCCAACTGCCATGTGGAAG
AGGTGCCCTCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTGAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCC**TAA**CCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTACGGCCCCACCCTTATTGATTCGT
ATCAGCTCTGGAGCAGAGGCAGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAATGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGTGTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGGTCACTGTATCTGAAGCCCTCGGAATAAAGCGCGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAA

00978194-101501

<subunit 1 of 1, 377 aa, 1 stop

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIKMTALELARRGAR
VVLACRSQERGEAAAPDLRQBSGNNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFFLLTHLLLPCLKACAPSRVVVVASAAHCRGLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTAAHPGPVNSELFLRHVPGLWRPLLR
PLAWLVLRAPRGGAAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLPGDEADPEDDPQSEDSEAPSSLSTPHPEEPTVVSQYPSPQSSPDLKSMTHRIQAKVEP
EIOLS

Signal peptide:

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATC**ATG**GGAGGCATGGCTCAG
 GACTCCCCGCCAGATCTAGTCCACCCCAAGGACAGCTGTTCAGGGCCCTGGCCCTCCAGGATGAGCTGC
 CAGGCTCAGGCCAGCCACCTCCACCATCCGCTGGTTGCTGAATGGGACAGCCCTGAGCATGGTGCCCCCAGAC
 CCAACACCACTCTCTGCTGATGGGACCTTCTGCTGCTACAGCCCTGCCCGGGGACATGCCACGATGGCCAG
 GCCTCTCCACAGACCTGGGGTGTCTACACATGTAGGGCCAGCAACCGGCTTGGCAGCGCAGTACAGCAGAGGCGCT
 CGCCTCTGTGGCTGTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGCTGGTGGGTGGAGCAG
 TTTACTCTGGAATGTGGGCGCCCTGGGGCCACCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTTG
 GCCTCCAGGCCGGAAGGACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGGATGACGAGAGG
 ACCATACATGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCATCCAGAGGCC
 CAGGACTACCGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTAGCTGGAAATTTGACATCTGCTCAACCCGGAT
 CCTGCAAGGGCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTAGTGGCCCTGCTGCCTGCCCTGCCAA
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGCAGAGGAGCTGCTGGCC
 GGTGGCAGAGCGCAGAGCTTGGAGGCTCCACTGGGGCCAGAGCTACGAGTTCAAAGTGAGACCATTCTCTGGC
 CGGCTCGAGGCCCTGACAGCAACGTGCTGCTTGAAGCTGCCGGAAAGTCCCACTGCCCACTCAGGAA
 GTGACTCTAAAGCCTGGCAATGGCATGTCTTTGTGAGCTGGGTCCCAACCACTGCTGAAAACCAATGGCATC
 ATCCGTGGCTACAGGCTTGGAGCTGGGCAACATCACTGCCACCGCCCACTGGACTGTAGTTGGTGAGCAG
 ACCAGACTGGAAATGCCCAACCATATGCCAGGCTCTACTGGGTGCAAGTGGCTGCAGTCACTGTGTCTGGAGCT
 GGGGAGCCCACTGAGCACTGTCTGCCCTCTTTAGAGCAGGCCATGGAGCGAGCCACCAAGAAAGCCAGTGAGACT
 GTGCTCTGAGCCCTGGAGCAGTGGGGTACTTGAAGCGGCTGAGGTCATTGGCCAGTGCGGTGTGGCATCT
 TGGCTGCTGCTTCTCGGACCCGCGGTGTGTATCCACCGCGCGCGAGCTAGGGGTGCACCTGGGGCCAGGTCTG
 TACAGATATACAGTGAGAGATGACCTCTAAACACAGGATGGATCAGAGTACTCCAGTGTGGGACACAT
 TGGCGTTCACCTCTGGCTCTCGGACCTGAGCAGCAGCAGCAGCTCAGCAGCTCGGCTGGGGCGGATGGCCGG
 GACCCACTAGACTGTGCTGCTGCTTGTCTCTGGGACTCCCGAAGCCCGGCTGGCCCTGCTCTCAGACACC
 AGCACTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCAGCT
 GTCAGGCGCTCCCACTGAGCTGGCCAGCTCTCCAGCCCTGTTCAGCTCAGACAGAGCTCTGCAAGCCGAGG
 GGACTCTTCTCCCGCTTGTCTCTGGCCCTGCAAGGCTTGAAGGCCAAAAGAAGCAGGAGCTGCAAGCAT
 GCCAACAGTTCCTCAGCTCTCCGGGGCAGCCTCTTGGAGCTCCGGGCTGTGAGTTAGGAAATAGAGGTTCC
 AAGAACCTTTCCAAAGCCAGGAGCTGTGCCCAAGCTGTGTTGCTGGCGGGCCCTGGGACCGAAACTCCTC
 AGCTCCTCAAAATGAGCTGGTTACTCTGCATCTCCCTCCAGCACCCCTCTTCTCATGAAACTCCCCAACTCAG
 AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCATCTGCTGCCAGCAGCCCCATCCCCATC
 CTTAGCCCCCTCAGTCCCCCTAGCCCCCAGGCCCTCTTCCCTCTGCGCCAGCCAGCTTCCAGTCCGCTGTCC
 AGCTCCTCACTGTATCCTCGGGGGAGGATCAAGACAGCGTCTGACCCCTGAGGAGGTAGCCCTGTGCTGGAA
 CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCTTCAACCCCCAACACTAT
 GGTACATCAGCGTCCCAACAGCTCAGAGTTTACAGGACATGGGCAAGGACTGGAGAGGGGTGGGGCCCAAGGGG
 GGAGTCTTGTGTGTCCTCGGCCCTGCTCACCCCACCCCGAGGAGGGCTCTTACCAATGGTTGGGGC
 TCAAGCTCTGAGGACAATGCGCCAGCGCCAGAGCCAGCCTTGTGAGCTCTCCGATGGCTCTTCTCTCGTGTAT
 GCTCACTTGGCCGGGCCCTGCGAGTGGCTGTGGATAGCTTGGTTTCGCTGAGTGGAGGAGGAGCAGACTGC
 GTCTTCATAGATGCTCATCACTCTCCCTCCCAAGGGATGAGATCTTCTGACCCCAACCTCTCCCTGCCCTTG
 TGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTACGACACCCAGCGCTGGGAAGGGGGATGCCTCC
 TGGCCCTCTGACTCTCAGATCTCTTCCAGAGAAGTCAAGTCCACTGTGCTGATGGCCCAAGGCTGGTCTCTCT
 GTAGATTCTCT**CGA**AGAGCTGCTGAGACTTCCAGAGCGGGAATCAGAACTCATCTCTGTGACCCCAAG
 ACCGTGGGCTGTGTGTGTGGGTCTTGGCCTGTGTCTTCTGCAAGCTGGGGTCACTCTCCCAAGCCTCCAGAGAG
 TTTCTCCCTCAAGATTGTGAAGACAAATGAACAAAAATTAGAGCAAAAGCTGACCTGGAGCCCTCAGGAGGCAAA
 ACATATCTCCACCTGACTCTAGCCACTGCTTTCTCTCTGTGCACTCACTCCCAACCAAGGTTGTCTTGGC
 CTCAGAGCAGCCCTGCTGCTGCTCTTCTCCCAACCAATTGGATCAGAGGAAGTGGAGGAGCAGAGGCTGCTT
 GTGGAGGACAGCATGGCTGCTGGGAGAGGCTGTGGAGGAAGGAGCTTCTGGAGCCCCCTCTCAGCCTTACCT
 GGCCCTCTCTAGAGAAGACTCACTCTCTCCCAACCTCCAGTGGAAAGAAATTAATTATGAATGCCACTG
 AGGCACTGAGGCCCTCACTCATGCCCAACCAAGGTTCAAGGCTGGGTCTAGCGAGGATCTGAGGAGGAGGAG
 TATGAGACCGTAGGTCAAGAGCACCATCTCTGACTGTGTCACTATGAGCTTAAGAAATTTGATACCATAAAT
 GGTAAAAA

09976144-103501

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLLP
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGFPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARA EKSD EGYTMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLRLEPKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSPTPARSPQVPVAVRRLPPQLAQLSSPCSSDSLCSRRLGLSSPRLSLAPAEA
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHTPTTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGVLLCPPRPCLTPTPSEGLANGWSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPVDS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGTATGGGGTTGCTCTGTGCT
CCGAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTGGAAGGGGACACTGTGT
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
GGGATCCTCTTCTCTCGTGTCTTGGCACCATTATGCAGAGAAGGAAGGCCAGGAGACAAT
GAAGGCGCAGGGTCTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
TCTTTACTGATCTCTGTTCGTCTTTCCAGGACCCTGCTGTCTCTCTCTCTCTCTCTCTCCAC
CTTCCAGCCTCTGGCTACAACACGCTGACGCCAAGGCAAAAGCTCAGCAAAACCAGCCCC
CAGGATTGACTTCTCTGGGGTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
GCTGAGGCCCTCCATTGCCAGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
AGGAACCTCTCTCTCACCAGCGACCTCTCTCTCTGACGGGAGCTCCCGCCCCCATGACAG
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
GTGTCCATCCCGATGGTCCGCATACCTGGCCCCAGTCTCTGGTGTCTGTGAGCCCTTCTGTGAGC
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAGGAAGCC
CCTTCCAGCCCTGAGGGGGACGTGATCTCGATGCTCTCTCTCCACACATCTGAGGAGGCA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGAGTACAGCACCAGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG
TCCAGCTGCCCGGACTCCAGGGCTCTCCCACTCCCGAGGCTCTCTCTTGCATGTTTCCA
GCCTGACCTAGAAGCGTTTGTGAGCCTGGAGCCAGAGCGGTGGCCTTGTCTCTTCGGCTG
GAGACTGGGACATCCCTGATAGGTTCAATCCCTGGGCAGAGTACAGGCTGCTGACCCCTA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
CTCATGCCAGTGTGGGACCCTGCTCTCTCTCCACTCCAGACCCCACTTGTCTTCTCTCTCT
TGGCGTCTCAGACTTAGTCCACGGTCTCTGTCATCAGCTGGTGATGAAGAGGAGCATGCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAAGAACCT
GTGAAAAACGTGATTCTGGGCCCAACAGACCCCAACCAATCTCTGGGCTTGGTGACAG
GACTCTGAATTCTAACAATGCCAGTACTGTGCACTTGAGTTTGAAGGCCAGTGGGCCCTG
ATGAACGCTCACACCCCTTACGCTTAGAGTCTGCATTGGGGCTGTGACGCTCTCCACCTGCCC
CAATAGATCTGCTCTGTCTGCGACACCAGATCCAGTGGGACTCCCTGAGGCCCTGCTAAG
TCCAGGCCTTGGTCAGGTGAGGTGCATTTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
TTGCCCTTNCATTGCCCCCTCCCTGGNCCATGCTTCTTGCTCTTTGAAAAAATGATGAAGA
AAACCTTGGCTCCTTCTTGTGCTGGAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAAACAGAGTGACGCTAGGTGTCTAAACACAGAGGAGTAGGAACAGGGCGG
ATACTGAAGGTGACTCAGGATCCAGCCCTCGAGGAGGGGTGGGGGTGGTGGTAAAGTA
GCACAATACTATTTTTTTTCTTTTTCCATTATTATTGTTTTTAAAGACAGAATCTCGTGCT
GCTGCCAGGCTGGAGTGCAGTGGGCACGATCTGCAAACTCCGCCCTCTGGGTTCAAGTGATT
CTTCTGCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGACACCACTGCTGCTTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTCACTATGTTGGCCAGGCTGGTCTTGAATCTCTGAC
CTCAAAATGAGCTCTCTGCTCTCAGTCTCCCAAATGCGGGATTACAGGCATGAGCCACTGTG
TCTGGCCCTATTCTTTTAAAAAGTGAAATTAAGAGTTGTTCAAGTATGCAAACTTGGAAAG
ATGGAGAGAAAAAGAAAAAGGAAGAAAAAATGTCAACCATAGTCTCACCAGAGACTATCAT
TATTTGTTTTGTTGTACTTCTCTTCCACTTTTTCTTCTTCTCATAAATTTGCGGGTGTCTT
TTTACAGAGCAATTATCTGTATATACAACCTTTGTATCTGCTCTTTCCACCTTATCGTTCC
ATCACTTTATCCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA
GCTGCATAAAAAA

00073194.101501

FOR THE RECORD

<subunit 1 of 1, 332 aa, 1 stop

MRLVLVLLWGCLLLPGYEALGPEEISGFEGDVTSLQCTYREELRDHRKYWCRKGGLFSCRCS
 GTIYABEEGQETMKGRVSIIRDSRQELSLVITLWNLTLQDAGYWCWGEKRGPDSELLISLFFV
 FPGPCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSFGLYPAATTAKQKGTGAEPPLFG
 TSQYGHERTSQYTGTSPHPATSPFAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPIVMRI
 LAPVLVLLSLLSAAGLIAFCPSHLLWRKEAQAQTETQRNEKFWLSRLTAAEKEAPSQAPEGD
 VISMPLLTSEBELGFSKFVSA

Signal peptide:

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGACGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

[illegible]

<subunit 1 of 1, 146 aa, 1 stop

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNIGIFQINSRRWCNSLTPNVPNVCRMYCSDLNPNLKDITVI CAMKITQEPQGLGY
WEAWRHHCQCKDLTEWVDGDCF

Signal peptide:

N-myristoylation site.

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCCGGGCCGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCTGCGTTCC
GCTGCGCCTCCTCGTCTTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCCA
AGCTGTCTGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGAAACCGGCGCTGGAAC TGCTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCTGCAGCAGTGGGGAGCT
GGAGAAGTGC GGCTGTGACAGGACAGTGATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAAATCGCCTACGGTGTGGCCTTCTCAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCTCGTCCAGCAGAGCCCTCATGAACCTCCACAAATGAGGCCGGCAG
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTGAGCTCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTA CTGTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTCTGGGCACAGGGGCGGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCGCGGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGCTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATTGACGCGCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACACCCTACCCCAAGA
GATACTGGTTGTATTTTTTGTCTCGTTTGGTTTTTGGGTCCCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACC AACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTGTCATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCAACCCCTCTGGA AAAAAGAACTCTTAACCTCTCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAAG
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCAATTTAGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCCTAGAACCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAAACTTAACTACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGCTGTGCCCTT
TGCAGTCATGCCCAGTCACCTTTACAGCGCTGTTCTCTCATGAAACTGAAAAACACACAC
ACACACACACACACACACACACACACACACACAGGACACACACACACACCTGCGAGA
GAGAGGGAGGAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTCT

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFVAFVSAASNWLYLAKLSSVGSISEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRWNCSTLDSLFPVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSEVKTWCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTGGTC
ACCACAGTCTCTTTGGGCTGTGATTCTGAGTATCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGCGCTGG
GTGCCCTGAAGGAGGAGGTTCGGAGACTGCCACAGCTGCTGCTCGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCTGAGG
GCTGTGCGCCATCTGGGCAAGTTTCAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGCGCGAGAACTGTGTCTATGATGC
TGCACACGGGGCTGTGGAACGACGCCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACCTGCTTGACCCCGCCCAGTGCCCTGGAGCCGCGCCCAATTGCAGCATGTCGTA
TCCTGGGGGTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT
CATCCACCGTGTGAGTCTCAGAAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTTGGTTTTCTCGCATTTTCCACCAAACTGGA
AGCTGTTTTTGACGCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

03976194-101501

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTRYSKWGGSSSEVPGGPWGRVWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVVTQGLAEAGRGREDVTELFRALAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLEQGFLLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEFNDAWGRENCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCGCAGCCCTTCTCCTCCTTTCTCCACGTCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCCGGCCCCG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGTGCTCTGCCGGGTGATGGAAAAACCCAGCCCGGCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCTGGCCACTCTCGGCGCCGCCGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCAAGCAGTACCCCTGTTCGCCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACAGTACGTACGTAACGGGCTGCG
CGACTTTGCGGAGCGCGCGAGGCCCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCGCGCTCCCAAGCGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCATCGTGCC
CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGCAGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCGGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCAG
CCACCCGGCAACTCCTTCTACTACCCGCGGTGAAGGCCCTGCCTCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGTCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTTCGTCTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGTCCAGCCCGCAACAACGGGAGCCCTGCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGACGCCCTGGGGCCCCCG
GAGCCATGGGGTGTGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTGGGAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCTGAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGTGCTCCAGGAGATTGTCTTCATCG
TCCAGGGGCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTGTCTAGGCTGTGCTG
AGCCCACTCTCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0976104.10504

FIGURE 87

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35844, pI: 5.45, NX(S/T): 2
MENPSPAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVSPDWFVGVDSLDLCDGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRGLGKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV
```

Important features:

Signal peptide:

amino acids 1-26

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCTGTCTTGCGTGA
TATTGACAACTGAAGCTTTCTGTCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACCTTTGTTTGGGAAGCTTATTATGACAATACCATTTTTATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTTCATTACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACTGGGTGAGCAGATGAACT
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTGAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCGAAGGAAATTTAAAGGCTGAAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGTTGATGAAAAGAAGCTGATGAGAGAAAGAATTGCCAAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTTAAACCGGGAACTCTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGAAGATCAGACCCTTGCACTGCTGAACCAAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTACATGTACTTCAGTTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAAGAAAGAATAAAT
GAGAATAATGATAACCAGAACTTGCTGGAATGTGCCTACAATGGCCTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTAAGAAAGAGTATTTTTGAACCTGTTGTCTGTTTTG
AAAAACAATTATCTGTGTTTGCAAAATTGTGAATGATGTAAGCAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTC
TCCACAAAAA

FIGURE 89

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPNPFDDIIPREIKRLKKEK
PEEEVKKLKPVGTKNFSLLSFGEAEAEAEAEVNRVSQSMGKSKSSHLLKDDPHLSSVPVV
ESEKGDAPDLVDDGDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKS
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDTFEYIDPRNPVNKRREESKKLMREKKERR
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCGTTGCCGGGCGAGAGAGATGCTGCCCGG
 CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCCGCCTTGCTGACGGCGCTCG
 AGCCCTTGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
 GTGGCCGCGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAAACGGGAACGCTCTAGCAA
 CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGAAGTACTTCAACTCCAGCAACTACATCTG
 CTCCTTCAAGTGGTTTTTGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
 GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC
 CCTGCAAGGAAAAACAGATGCATGTGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTT
 TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAA
 GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTCCGACAGGCTGGAG
 TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCCTCCGGGTTCAAGCGAGTCTCTCTGC
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGACGAGTCTCTGGGGCCAGCTGGGCTCTG
 ATGTACGTGAGCACGCGGGGAACGGTACAAGTGGCTGCGCTTCAAGGAGGACTGTCTGTACCT
 GAACGTGTACGCGCCGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
 CGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC
 GAGAAAGTGGTGTGGTTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGA
 CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACAGATGGCGGCTCTGCGCTGGGTGC
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCTTCTCGGCCAGTCCGCG
 GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC
 CATTTCCAGAGTGGCACCGCGTTATTTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
 CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACACAGCACACAGATCCTGGTAAACTGC
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCTCAACT
 GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
 TGATCCAGATGACCCTTTGGTGTCTCCTGACCCAGGGGAAGGTTTCATCTGTGGCCCTACCTT
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCCTTATAATATCACCAAGGAGCAGGT
 ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCTGTATGCCACACTGCAGACTGCTCAC
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGTCTGGCCACGCTACACAAGGATGAA
 AAGTACCTGCAGCTGGATTTTACACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
 TTTTTGGATGAGTCTGTACCAGTCTCAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
 TATGCAGGAAGGACCAAGAGGGGTTTGCCCCACCATTCCAGGCCCTGGGGAGACTAGCCA
 TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAAGTGCAGGAGCTCCCTGCT
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCTGTGTGTGGGACCTGCAGCTGCCCTTTCCAGCC
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACTCTTTTTTTCCCTTCTTCAATCCT
 CCCACCCCTTCAATGTCTCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCCCTGC
 CCCTGTCACTGCACCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTCTCTGTCTGT
 TCACATTGGCCTGGAGGCTTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA
 TCTCTCTCCACCACTATTCTCCCCAGGGCCACTCAAAGTCTATACACAGGGGTGG
 TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

090708797.104507

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVFPFSRPP
LGILRFAPPEPPEPFWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWQLASMYVSTREYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLLSTDDSHARGNWLGLDQMAALRWVQENIA
AFGGDPGNVTLLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCRLALSGTKVMRVSNKMRFLQLNFQRDPPEEIIWSMSPVVDGVVIPPDD
PLVLLTQKGVSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGTCT
 GCTGTCCTCGCTGCTGGGCGGGTCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
 AGTCAGTGATGGTGCCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGCA
 CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAGAGCAGTGACTGAGACAAC
 CAAGGGTGTCTCTGTGGCCACAACCCACAGAGTCGAGAGGTTGGAATGAGCACCCGGGGCC
 GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAACGTCTCCTTGGTGATCAGAGACGCGCAG
 ATGCGAGGATGAGTCACAGTACTTCTTTGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
 CATGAACGATGGGTTCTTTCTAAAGTAACAGTGCTCAGCTTTCACGCCAGACCCAGGACC
 ACAACACGCACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
 GTCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTTACGTGACAACAC
 GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCATACCTGGAAGCCCAAAAGGCCAGT
 TCCTGCGGCTCTCTGTGTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGTGAG
 AACAGAGTCTCTCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
 GGTGAAGGCTGGGGATTACAGGCGCTACACCTGCGGAGCGGAGAACAGGCTTGGCTCCAGC
 AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCAA
 GCAACAGGACAGCTCTGGAAACCTTGGAAACGGCACGTCCTTCCAGTACTGGAGGGCCA
 AAGCCTGTGCGCTGGTCTGTGTACACACAGCAGCCCCCAGCGAGGCTGAGCTGGACCCAGA
 GGGCAGAGGTTCTGAGCCTCTCCAGCCCTCAGACCCCGGGCTCTGGAGCTGCTCTGGGTT
 CAAGTGGAGCAGGAAGGAGAGTTCACCTGCCAGCTCGGCACCCACTGGGCTCCAGCACGT
 CTCTCTCAGCCTCTCGGTGCACTATAAGAAGGAGTCTATCTCAACGGCATTCTCCAACGGAG
 CGTTTCTGGGAATCGGCATCAGCGCTCTTCTTTCTGCTGCTGGCCCTGATCATATGAAG
 ATTCTACCGAAGAGACGGAATCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAC
 GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
 AAGCCACACCAACAGTCTCTCGGACCCCTCCTCCACAGGCTGCTCCCTCCCAAGATCAAAG
 AAGAACCAGAAAAAGCAGTATCAGTTGCCCAAGTTCCCAAGAACCCAAATCATCCACTCAAGC
 CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCA
 GACCCAGGCTGAGGCCGGATGCCCAAGGGCACCAGGCGGATTATGCAGAAGTCAAGTTC
 CAATGAAGGTTCTTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
 GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTTTCTCTCTCTCT
 CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCTGTGAATC
 CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTCGGGAGTTCGAGACCAGCCTG
 GCCAATCTGGTGAAACCCCGTCTCTACTAAAAATACAAAATTAGCTGGGCGATGGTGGCAGG
 CGCCTGTAATCTACCTACTTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
 AGGTTGAGCTGAGCCAGATCACACCATTTGCACGCCAGCTGGGCAACAAAGCGAGACTCCA
 TCTCAAAAAAAATCCTCCAATGGGTTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTA
 AGGTGGGTGGATTGCTTGAGCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAACCCCT
 ATCTTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCTGCTGTAGTCCAGCTGT
 CAGACATTTAAACAGAGCAACTCCATCTGGAATAGGAGCTGAATAAATGAGGCTGAGACC
 TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGATGAGACAGGAGTCCG
 TACAAGATAACAGGTATAAAAGACTTTGCTGATAAAACAGATTGCAAGTAAGAAAGCCAAACCA
 ATCCCAACCAAGCAAGTTGGCCACGAGAGTGACCTCTGGTCTGTCCTCACTGCTACACTCT
 GACAGCACCATAAGCAATTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATTTGTCCCA
 AAAGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAATAAGCAAGAAATAACCATAAAA
 GTGGGCAACAGCAGCTCTAGGCGTGTCTTGTCTATGGAGTAGCCATTCTTTGTCTCTT
 TACTTTCTTAATAAACTTGCTTTTCACTTTAAAAAAA

0973104-107501

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1 stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLP L L L S S L L G G S Q A M D G R F W I R V Q E S V M V P E G L C I S V P C S F S Y P R Q D W T G S T P A Y G Y W F K
A V T E T T K G A P V A T N H Q S R E V E M S T R G R F Q L T G D P A K G N C S L V I R D A Q M Q D E S Q Y F F R V E R G S
Y V T Y N F M N D G F F L K V T V L S F T P R P Q D H N T D L T C H V D F S R K G V S A Q R T V R L R V A Y A P R D L V I S
I S R D N T P A L E P Q P Q G N V P Y L E A Q K G Q F L R L L C A A D S Q P P A T L S W V L Q N R V L S S S H P W G P R P L
G L E L P G V K A G D S G R Y T C R A E N R L G S Q Q R A L D L S V Q Y P P E N L R V M V S Q A N R T V L E N L G N G T S L
P V L E G Q S L C L V C V T H S S P P A R L S W T Q R G Q V L S P S Q P S D P G V L E L P R V Q V E H E G E F T C H A R H P
L G S Q H V S L S L S V H Y K K G L I S T A F S N G A F L G I G I T A L L F L C L A L I I M K I L P K R R T Q T E T P R P R
F S R H S T I L D Y I N V V P T A G P L A Q K R N Q K A T P N S P R T P P P P G A P S P E S K K N Q K K Q Y Q L P S F P E P
K S S T Q A P E S Q E S Q E E L H Y A T L N F F G V R P R P E A R M P K G T Q A D Y A E V K F Q

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins
signature.**

amino acids 365-371

007404-0000

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAACCTGTTATTTACTGCTGCGTTT
 TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACTCTCAAACAAAGA
 AAGTCAAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
 TTTGTACCAGAGGAAATGAAATACGACTAGTCATCATCGGCCAGCTAAGATCTGATTTTGA
 CAATGGAAACAATTCCTTCAGTACAAGCTTTTGGGAGCTGGAGCTGGAGTACTTTTATCA
 TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
 TACATCTTAAGAGCCAGGTAAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
 GTTTTCTCATCAAAGTTTTCGGATATCAATGACAAATGAACCAAAAATTCCTAGATGAACCTTATG
 AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAGAGTGAT
 GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
 ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAAATGGATAGAGAAC
 TGCAAGATGAGTATTTGGGTAACTATTCAAGCCAAGGACATGATTGGTCAAGCCAGGAGCGTTG
 TCTGGAACAACAAGTGTTAATTAATAACTTTCCAGATGTTAATGACAATAAGCCTATATTTAA
 AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
 GATTGCAAAACATTGACATTTACTAATCATGAAACTCAAGAAGGAATAGTTTATATTTAAA
 AAAGAAAGTGGATTTTTGGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAACCAATC
 ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAG
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTGTGA
 AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACATAGGAAAT
 CTCCTATCAGGTATTCTATTACTAGGAGCAAAAGTGTTCATATCAATGAATAAGTATGATCAATC
 ACTACAAGTAACTCACTGGATCGTGAAATCAGTGTCTGGTACAACCTAAGTATTACAGCCAC
 AGAAAAATACAATATAGAACAGATCTCTTCCAGTCCACTGTATGTGCAAGTTCTTAACATCA
 ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTAAAAATGACGGCTCT
 GGTCAAGTAATTGAGATCATGATGCAAGTGGATAGAGATGAATCCATAGAAGAGCACCATT
 TTACTTTAATCTATCTGTAGAAGACACTAACAAATCAAGTTTAAATCATAGATAATCAAG
 ATAACACAGCTGTCAATTTGACTAATAGAACTGGTTTAACTTCAAGAAGAACCTGTCTTC
 TACATCTCCATCTTAATTGCCGCAATGGAATCCCGTCACTTACAAGTACAAACACCCCTTAC
 CATCCATGTCTGTGACTGTGGTGAAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
 TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTCATTTATGATCATAT
 TTTGGGTTTATTTTCTGACTTTGGGTTTAAAAACAACGGAGAAAAACAGATTTCTATTCTGA
 GAAAAGTGAAGATTTTCAAGAGAAATATATTTCCATATGATGATGAAGGGGGTGGAGAAGAAG
 ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAAACGCAAGACT
 CGGAAAAACCAAGCGCTGAGATCAGGAGCTTATACAGGAGCTTTTGAAGTGTGGCCAGTTGGCCCGCA
 CAGTGCCATATTCAAGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
 CCCCTCCTTTTGAATTCCTCCAGACCTACGCTTTTGGGGAAACAGGGTCATTAGCTGGATCC
 CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
 GGGACCTCGCTTAAAAAGATTAGCATGCATGTTTGGTTCTGCAAGTGCAGTCAAATAGATTAGG
 GCTTTTACCATTAAAATTTTAAAAAGTGCTAATGTGATTTCGAACCCAAATGGTAGTCTTAA
 AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTCTGATTTCC
 CTGGAGTAAATCTCCATGGTTATTTAAAGCTACCTACATGCTGTGTCATTGAACAGAGATGTG
 GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACAGGATTTGAAGTAAATTAATG
 TAGGAAGATATTTAAAGTAGATGAGAGGACACAAGATGTAGTGCATCCTTATGCGATTATAT
 CATTATTTACTTAGGAAAGAGTAAAAATACCAACAGGAAAAATTTAAAGGAGCAAAAATTTG
 CAAGTCAATAGAAATGTACAAATCGAGATAACATTACATTTTATGATCAATTTAGATGAAA
 ATTGAAAATGTATAGTCAGAGAAATTTTATGAATTATTCATGAAGTATTGTTTCTCTTAT
 TTAAA

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FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLPCLGATENSQTKVKQFVRSHLRVKGWVWNQFFVPEEMNTTSHH
IGQLRSDLNNGNNSFYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLQGQPYFSVEPTTGVIIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKP I FKESLYRLTVSESAPTGT SIGT IMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNLDREISA
WYNLSITATEKYNIEQISSIPLYQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESEIEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEBANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESASVSDQD
ESYDYLNLGLPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 96

ATTTCAAGGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTGCGAAACATTTGACATTATT

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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI¹LAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQI
QCKVFD²SLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDD³EVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTFVNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTTSYPTPRPYPKPAPSSGKD⁴YV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGC AAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTG CAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCATGACCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

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FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGGAAGACGATGA
GGTGCGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTCTGCAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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GGGCCCGACCAATTATCCAACGGGNTCACTGTTGGTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTNNCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTGCGGTGTCGAGANACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCNTGCCCCGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGATGAAGT
GCTTGGGAAGCAGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTGTCTGTTCTCTGCGA

FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCCGTGCC

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FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNCCACAGCAT
GGTATGGCAATAGNATNNTTGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTGTCCCCGAA

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AGCAATGCCCTGCCCCAGTGGAGGATTAATTCTATGNTGGGACAAACATTGTGACNCGCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGACACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGACATTTGCAAGCAACCCTGCGCCTTGATGGT
GGTTGGCATCTTCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGATGA
AGTGCTTGAAGACGATGAGGTGCGAGAAGATGAGGATGGCTGTATTGGGGGCGCGATATTT
CTTNTTGCAGGCTGTGGCTATTTTAGTTGGCACACGACATGGATATGGCAAGATNTGTTCAAGA
ATTTTATGCCACCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
CTGGGCTGCTGCTTNTTTCTGCTTNTGGGAGGTGCCANTTTGCTGTTCCTGCGAACCC

FIGURE 105

TCATAGGGGGGCGGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCCTATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTGCTGTTCCTG

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FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCATGACCCCAAGTCAATGCCAGGTA
CGAATTGTGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTCTGTCCCGAAAAACAACCTCTTACCCACG

FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNCGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCGCTTCTGGGAGGTGCCCTACTTTGCTGTTCCCTGCGAA

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA

FIGURE 108

GCGTGCCGTGAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCGCCCTCGCCCTGAC
 CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCTCG
 ACCGGTCCCCGCTTTTGTAAACTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCGGT
 GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCGCCCGCTAAGGAACATGGCGAAGGTGGAG
 CAGGTCTGAGCCTCGAGCCGCGAGCACGAGCTCAAATTCGAGGTCCCTTCAACCGATGTTGT
 CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTTGTGTTTTAAGGTGAAGACTA
 CAGCACACGTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCAAGGGGCTCAATT
 AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAAGTAAACAAAGTT
 TATGGTTTCAGTCTATGTTTGTCTCAAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
 CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
 GATAAACCCACATGATGTAGAAAAATAATAAAATTATATCCACAACCTGCATCAAAAGACAGAAAC
 ACCAATAGTGCTCTAAGTCTCTGAGTCTCTTCTTGGATGACACCCGAAGTTAAGAAGGTTATGG
 AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAAGGCTACGGGAGGAGAACAAAGCAGTTCAAG
 GAAGAAGATGGACTCGCGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC
 CCAAACCTGGGAAGGAAGAAGGCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA
 TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCAAGGATGGTAAATTG
 GATTTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAAACCATGTGTAAGAAAGAAATT
 AATGTATGATGACATCTCACAGGTCTTGCTTTAAATTACCCCTCCCTGCACACACATACAC
 AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAAGTTAAAAATGTATAGTAACTG
 ATTGAGGGGGAAAAAGAAATGATCTTTATTAAATGACAAGGGAAACCATGAGTAATGCCACAAT
 GGCATATTGTAATGTCTATTTTAAACATTTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC
 TCTTAAATGACACCCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCAGCAT
 GCTGGGGAGTGGCGTCAGCTCCACACAGTAGTCCCACGTTGGCCCACTCCCGGCCAGGCTG
 CTTTCGCTGCTCTCAGTTCTGTCCAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
 AGCCCCAAAGGAATTGCATCTGTGCGAGCATCAGACGTACTCTGCATAGTGAAGGCGGTGTGT
 TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACCTTAAAGGGACCAA
 GCTAAATTTGATTTGGTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAAATGCA
 TTTAACTTATTTAATGTATTTTCATCTCATGTTTCTTATTGTACAAAGAGTACAGTTAATGC
 TGCCTGCTGTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCTCT
 GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
 GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAATTTCTCAGTAGTG
 ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTCTCTAGATTGTTCTTATA
 CCACCTCTCAACCATTAACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
 TTGGGACCTAGCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGGAGGC
 ACCAGCAGTTGTGGGTGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
 TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
 CTATGTAGCATCTTGAAGAAAGAAATTTATAATAAAGCCCCAAATTAAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977
<subunit 1 of 1, 243 aa, 1 stop
<MW: 27228, pI: 7.43, NX(S/T): 2
MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQPFDYDPNEKSKHKFMVQSMFAPTDTSDEAVWKEAKPEDLMSKLRGVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCC
CCAAAATTAAGAATTCCTTTGTCAATTTGTCAATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTATTATTTTGGCATTGGAAGGTTAACTTTAAAATGAGC

FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGT CAGCTCCACACAGTAGTCCCCACGTGGCCCCACTCCCGGCC CAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTCTTATTCAGAGATGTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTCTTATTGT CACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAAATNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

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FIGURE 113

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTCAANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTG
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAAC TGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

097834.04504

FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAAATGC
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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105044-1050

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAAATGACAAGGGAAACNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGGCCANTCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTATTTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTCAINTCATGTTTCTTATTGTACAAAGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGC GGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTTCGGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACCTCTGTTGGGTGAAC TGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

FIGURE 117

GCAGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCGGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGGC
CTCGGGGACCAAAACAGCCTGCGAGGGTCTCAGTTTGTGTGCCAGGCTGGAGTTCACTGCCA
TGATCATGGTTTACTGCGACCTTGACCTCCTGGGTTCAGCGGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTTCAAC
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCAGCTTGAGAAA
GGTACCCCGGATTGTCACTGAAAGGACTTTCCATCTCACCAGCCCCGATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCAGC
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAAATGGCACCCGAACTTT
AACCAGGGTGAAAGTTCAAGATTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTACGATCTTGGACAAA
AGGTTCTTAAACAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCTCAGCATGTCTTAAGTGTGCTGCCACTGTGTTCATGATGAAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTGTGTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGCTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAAGAAAATCTGGCCGGGGTC
AGAGGATTGCCGAAGGGGAGGCCCTTCTTTTCAGTGGACCCGGGTCAAGAATACCCACATTCGG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAGAAAGAAATACATGGAAGTTGGAATCAGCCCCACGATCAAGAAAA
TGCCTGGTGGAAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGTATCAGTTGGTCTAT
CGGTTTTGCAAGTGTGTCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTTCGGGGGCTATCTGCGTCTGAAAGATCCAGACAAAAGAAATTTGAAGC
GCAAAATCATTTGCGGTCTACTCAGGGCACAGTGGGTGGATGTCCACGGGGTTTCAAGAGGAC
TACAACGTTGCTGTTCCGATCACTCCCTTAAATACGCCAGATTTGCTTGGATTCAAGG
GAACGATGCCAATTTGTGCTTACGGCTTACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCTCGGACTT
GAACCTCTGTCAATAGCATTTCAACATTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATATCTTCTTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTATTAAATGTGAATTCATAGATATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTATCTGTTGGGTCT
GGGACATTTAGTTTAGTTTTTTGAAGAATTACAAATCAGAAGAAAGCAAGCAAGCTATATAA
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTGTCTATGAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTTAACTAATACTCAAAATATGGACTTTTTCATGTATGCATAGGG
AAGACACTTCAAAAATATGAATGATCATGTGTTGAAAGCCACATATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTTAGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGTTGAATTCCTGATTAG
TAATTTTATAGATATGCTCTTCTTCTAAAAATGAATAAAATTTATGAATATGA

COGNITIVE LINGUISTICS

<subunit 1 of 1, 413 aa, 1 stop

MENMLLWLIFFTPGWILIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFBADAAMMNVNTVC
 GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
 YGTDSRFSILDKRFLTNFFPSTAVKLSTGCGSLILISPHVLTAACHVDHKDYVKGSKKLRV
 GLLKMRNKS GGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRRKKSGRGQRIAEGRPS
 FQWTRVNKTHIPKGWARGGMSDANTLDLYYALLESKHLKRAHKKKMYELGISPTIKKMPGGMIHFS
 GFDNDRADQVLVYRFSVSGDESNLLDLYQCDAESGSGVYLRKLPDKKNWKRKI IAVYSG
 HQWVDVHVGQKDYNVAVRITPLKYAICLWIHGNDANCAYG

Signal peptide:

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AAATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCAACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCCTGGTGTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGCTCTGCAACGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCTGATCACTT
ATATCTGGAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAAAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTGTAACTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGAGGGGAGACGGATTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCATGGACCGCGTGCTCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGCATCCAGGGGCA
TGTCACTTCAGTGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCACTCCCTGCTATA
AACCCAAAGAGAAACTTCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGGAGCCCTCGTAAAGTTGTAAGAGCAGAGCTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTGTAGCTTTTCATGGGTTCTGA
ACTAAGTGAATCATCTACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA
AAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLFLFLLLSSRTARSEBEDRDGLWDAGPWSSECSRTC GGGASYS LRRLCLS
SKSCEGRNIRYRTC SNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNP CSLKQC
AKGTTLVVELAPKVL DGT RCTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLV LKGP D HLYLET KT LQGT KGENSL SSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTAD FIVKIRNSGSADSTVQFIFYQPI IHRWRET DFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDP CPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQEELEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

0997494-0051
1997494-0051

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCCTGGAGGGGCCGCTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGCGTTTCGTGGGGCCAGGGTCCAGCGGCTGCGCAGAGCGGGGACCCCGGCCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCGCGGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGTGATCATGGGCTGCCGGACCGCGCGCGCCGAGGAG
GCGGCGGGTCAGTCCGCCCGAGCTCCGCCAGGCCGCGGAGTGGCGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCTTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAGTTTCAGCTCCAGCA
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAAGTGGCTAACATTCTTTT
TACCAGGGAAGTACCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGTATGGGCTTTTTCAAAAGTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AAGTGTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAAGTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAAAGCAACAAGGAGTAAAGAGCTGTTTATAAAAGTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAAGTCTGTTACTTGAAGAAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT
TGGGATAAGAGAATTTTCAGCAAAGATGTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

0973134.104504

090709Z JUL 77

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
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<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPVRVQRLRRGGDPLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRRELRLQAACBGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEPRDLVLIINNAGIFQCPLYMKTEDGFEMQFVGNHLGHFLTLNLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEGNTVNTVNVLHPG
IVRTNLGRHIHILPLLVKPLNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEE
LLPKAMDESVAARKLDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGA ACTTGT TACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTT CAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGT CAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

0978194.101201

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTTCGGCTCCCGAGCCAGCC
CTTTCCTAACCCAAACCCAACTAGCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTACCGGAC
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACCTTGGGTTTTTACTCCTGTAACAACCTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAAATTTTGGGAAGCTTCCGATGTCATTAAAGGAAGAATT
TCCAATGAAAAATCAAGTAGTGTTCGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAAATACCCAACCTCAAATGTTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAGAAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTGGGGATGTTTCAAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT
GTCCGAGAAATAACATTTGAAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTAGAAATATTCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACTCCAGCAGATTGTCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTGC
TATTTGACTTACATCTCTGAAAACTGCACAGAGAATTCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAACTTG
AAAAACAGTTTGAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTA
TATTTTCATAATTCTATGTATTTTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09973194.104534

FIGURE 125

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAETITLDRSKRNIIIGYFEQKSDSNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELTEEGLPFLILFHMKEDESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL
```

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTTGGCAGATTA

09978194-101504

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCGNGGAGCCCGGGTCGAGAGGACNAGG
TGCCCGCTGCCTGGAGAATCCTCCGCTGCCGCTCGGCTCCCGGAGCCCAGCCCTTTCCTAAGCC
AACCCAAACCTAGCCCNCTCCAGCCGCCAGCGCCTGTCCCTGTCTCNGGANCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGCTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCTTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

0376494.101501

FIGURE 128

CCCCACGCGTCCGATGGCGTTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTGGGCACATTATAGCATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGAATACCTGAATCCCTTGTACTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCTCTTTGGCATAATCATATTTGGAGGTATATGAGTAGACCAGTGAAGTGGCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGATG
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTCCACATTTTGCCTTGTGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTGACAGGTTTGAACCTGCACCTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTGTGA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAATAAAAAGCGGGAATTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTATTGTGAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACCTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTTCCTTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

3978104.104504

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0
MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

FIGURE 130

ATTATAGCATTGTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAAATACCCCTG
AATCCCCCTTGTA CTCCCAGAGTACCTCATCCACGCTTCTTCTGTGTCATGTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATATTGGAGGTATA
TGAGTAGACCAGTGTAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
T TACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAAACACAGAAGAATT
GGTCCAGTTAAGTG CATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

09978194.101501

0 9 2 3 4 5 6 7 8 9

CGCAGCGCTGGGGGAAACCCCTTCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGCAGAGGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGGCTCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTTCGGGACCGCTTCGGCTGAAGCATTGTAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCACTGACCTACCCCTTGCACAC
CTACCCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTCAATTGTTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACCTGAGACAAGAACTTATGTCCCTGATGCCAAAATGCACCTACTCTTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTGAAGATGGA
GAAAGTGATGGCTTTTAAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT
TGTCTCTCGGTGATGGTATTGCTTTGGATTGTGTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATCTCCAGCTTCTCTCTTGTGGTTGTTAGATCTAAAATGAAGATCATGAAGA
ACGAGGGCATCTACCTACAAAAGTGAATCTTGTCTATTCTGAATTTAAGCATTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATCTCCACTCCTCATAGAGCTTTTAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCATATAAAATGCAATAAAGTTACTCAAACTCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTMALAGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP
KEEELYACQRCRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWS DMMSAQSFITSSWTFY LQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGF LRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

5576194.101504

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCTCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCG
TGAAC TGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

0973194-101501

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGCGCGGAGGTTGCGGGACCG
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTGCTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCACTCTGGAGTGACATGATGGACT
CCGC

0978194-104534

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGAGAGCTGCAATGGGCGCGGCTG
GGGAITCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCGGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCAATTGATAGATTTAATACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGCTCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGTATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATACTTCTGTGAAGCTGATGAC
ATTCACTCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAATAATGGAATGTCTACGAAGAAAAGCTGTTTTAAGCCAC
AGACAATTAAGAACCCTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACT
TTTTACAGTTGGCTAGAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGTGCCAAGAAGGCTTAAGAACTTGATTTTCTCTACTTAATAGAAGTAAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAATAAAATTC
AGGATGAGGAAAACAAAATGTTACTTCTGGAATACTTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTGTCTGGGGATAAAAAAGAAGCACAAAATAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGACCTAGTTATGAATTCCATCTAACCGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAGAATTAGAAAAT
TCAGGAACCTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGGAATTTCAATCAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACAATTTT
AAAAATGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAAATATTGAATAAAGGAGGATTATCAAATTAACAAAAA
AAAAAAAAAAAAAAAAAAAAA

0076194.10501

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974
<subunit 1 of 1, 468 aa, 1 stop
<MW: 54393, pI: 5.63, NX(S/T): 2
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAARQCFCQVSGYLDCTCDVETIDRFNNYRLF
PRLQKLLSDYFRYYKVNLRPCPFWNDSQCGRRDCAVKPCQSDEVPDGIKSASYKYSEEA
NNLIBECEQAERLGAVDESLSSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRLKNLYFLYLI
ELRLASKVLPPFFERPDLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGSPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

397649-1050

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTTAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTGATGGAATTTTGACTGAAGGAGAAGGTC CAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTCCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

0070104-101501

FIGURE 139

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSFFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW
DGPSGDRRGDVYRCVPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGFMVS
```

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

FIGURE 140

CACAGTCCCCACCATCACTCNTCCCATTCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAAC TCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTGTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCCACAATGCCCCATGTGTGCCAAGGGCCACTTAGGTGACTA
CCAAC TGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

0978194.104501

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCGGCTCTAGAACA
ATTTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTATGTGGTTTTTCT
ACGCATTGATTCATGTTTGTCTCAGATGAAAGTGCCACTTCTGCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
AACAGTGTACTATTCTGTGCAATACCGAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCAGTGTGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATGTAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
GGGTATTCCAGTGCACCTAGAAAACCTGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
CATTCTGTGAAGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTTCGTCTGAAAAATGGGCGGCTGCTCCAGTACTCCTGTGCCCCGTGG
TGGTCTCTCCAGACACCTTGAAAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAAG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCTGAGGAACTCCTCAGGGCCTGGAT
CTC**ATAG**AGTTTGCAGAGGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCATCTGTAATGGGGGAATTACC
TACACACCTGTAAACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTTCACAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAATGGGATGTGCATGAACACGGAGGATC
CATGAACACTAGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAATAAAAAAGGCCACCTGGCCAAAACGGGTAAAAAA
AAAAAAAAAA

09973194-101504

FIGURE 142

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033
<subunit 1 of 1, 311 aa, 1 stop
<MW: 35076, pI: 5.04, NX(S/T): 2
MQTFTMVLEEIIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPEDVTDITATVPYNLRVRATLGSQTS AW
SILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRRREP GAEHV KMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLV LALFAFVGFM LILV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS
```

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACTGAGTCTACCAAATGCAGACTTTCACAAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCTCAGAACCCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAAAGTGTACTATCTGTCTGAATACAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCTAGGGCCACATTTGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTCGCAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGTGAGTGGCGCTGGGTTGAT

FIGURE 144

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCCAGAAGGAGGGACAGAGGAGCTGAGAGAGGGGGGAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCAGAC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACACAGCCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAAACCCGGCCGACATGTCTCCTTCTGCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAATGCGGCTGTCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACAGGGCTTCTCTGTG
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTAGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCT
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTTCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCTGCAGCCCTTGGCCCCACAGGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCCCAGAGGCGCTGCCGAGGCCCACTACCGCCTGCATGTGGA
TGGTGTCCCCCATGGTCGCTGAGACTCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTC
CCCACAAGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTAA

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGKLRGTLTYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE
TVTILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGCGCCTGTTCTGCGCTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCGCCGAGCCTC
 GTTCTGTGTCCCCGCCCTCGCTCCTGCGAGCTACTGCTCAGAAAACGCTGGGGGCCCCACCTGGGCAGACTAACGAA
 GCAGCTCCCTTCCCAACCCCACTGCGAGTCTAATTTTGGACGCTTTGGCTGCCATTTCTTCCAGGTTGAGGGAGC
 CGCAGAGGCGGAGGCTCGCGTATTCTGCGAGTCAGCACCCACGCTCGCCCCCGAGCGCTCGTGCTCAGGCCCTTC
 GCGAGGGCGGCGCTCTCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCGAGGCCGCGCGCTGCGGTTTGGCT
 CACCTCTCCAGGAACCTTCACTGGAGAGCCAAAAGGATGGAGAGCCCTGTCTTGGAGATTTCTTGGGAGAA
 ATCTCAGGTCATTATTAGTAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCAAGTGTCTTATGGCTAGA
 GCAATTCAGCCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTGGAAAAATCATGGATGAGGATGGT
 GAGTGTGTGATAGCAAAACAAAGAGGAAAAAGGCCATCAGACCAATGACATGAGGATTTTGGACCTTCAT
 AATAATTCAGAACTCAGGTGATCTCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTGCAAGATCTGGGCTGAAAGTTGCTTGGGAAATGGAGCCTGCAAGCTTGTCTCCATCAATTTGGACAGAAT
 TTGGGAGCACACTGGGGAAGATATAGGCCCCGACGCTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
 AGCTACCATATGAACATGAATGCAACCCATATTGTCCATTCAGGTGTCTTGGCCCTGTATGTACACATATACA
 CAGGTCTGTGGGCAACTAGTAAACAGAATCGGTTGTGCCATTAATTTGTGTCAACATGAACATCTGGGGCGAG
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAGGGAACCTGGTGGGCGCATGCCCTTACAAA
 CATGGGCGGCCTTCTGCTGTGCCACCTAGTTTGGAGGGGCTGTAGAGAAAATCTGTGCTACAAAGAGGG
 TCAGACAGGATTTATCCCTCGAGAAGAGGAAACAAATGAAATAGAAGCAGACGAGTCACAAGTCCATGACACC
 CATGTCCGGACAAGATCAGATGATAGTACAGAAATGAAGTCTAAGCGCACAGCAAAATGTCCCAAATTTGTTCT
 TGTGAAGTAAATTAAGAGATCAGTGCAAGGAAACAACCTGCAATAGGTACGAATGTCTCTGTGGCTGTTGGAT
 AGTAAAGCTTAAAGTTATTGGCAGTGTAATTATGAAATGCAATCAGCATCTGAGAGCTGCAATTCATTATGTG
 ATATAGACAATGATGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTTTTCATCAAGTCCAAATAGA
 AATGGTATTCAAACAATTTGGCAAAATATCAGTCTGCTAATTCCTTACAGTCTCTAAAGTTAACAGTTACAGGCTGTG
 ACTGTGAAAACAACCTGTGGAACAGCTCTGTCCATTTTATAAGCTGTGTTCACTTCCCAAGATATCTGTCTCT
 CGTAACTGTATGCAAGCAAAATCCACATTATGCTCGTGTAAATGGAACCTCAGGTTTATTTCTGATCTGTCCAGTATC
 TGCAGAGCAGCAGTATGCTCGGAGTGGTTTCAAAATCACGGTGGTTATGTTGATGTAATGGCTGTGGGCAAAAAGA
 AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAATCTCTCAGGAGGAAAGGCATT
 AGAGTGTGTTGCTGTTGTGTAAGTCTGAATACCTTGAAGAGGACCAATAAGACTATTTCAAAATGCAATATTCTGA
 ATTTTGTATAAAAGCTGAACATTAAGTGTACAGAGTACATCAACTATTTTTCAGCCCAAAAGGTCGCAAAATGCATA
 TAAATCTTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTATGAAAATATAATGG
 TTTTAGAAATCTGTGTTAAATATTGCTATATTTTCTTAGCAGTATTTTCTACAGTTAATATACATAGTCATGATT
 GTTCTACGTTTCATATATTATATGTTGCTTTGTATATGCACTAATAAAATGAATCTAAACATTGAATGTGAATG
 GCCTCAGAAAATCATCTAGTGCAATTTAAAAATAATCGACTCTAAAACTGAAAGAAACCTTATCACATTTCCCC
 AGTTCAATGCTATGCGATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTCT
 TGTAAATTTAGGCATATAGAATATTAAATCTGATATGCACTTCTTATTTATATAAAATTAATCCTTTAATATC
 CAAATGAATCTGTTAAAAATGTTTGAATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGT
 ATGAAAACATTCCTAGTATCATGTAGTAAATGTAGGTTAAGCATGGACAGCAGAGCTTTCTATGTACTGTTA
 AAATGGAGTCAATATTTTCTTTTGTATCCTTGGCAAAATCTCTGACGGCAGGAAGTATTAATAGCAAAAAGTT
 GAACAAAGATGAACATATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTTGATATA
 ATATTGCCATATCATGGTACCATAAATGGTGATATATTTGTTCTATGAAAAATGATTGTGCTTTGATACTAAA
 AATCTGTAAATGTTAGTTTGGTAATTTTTTTCTGCTGGTGGATTACATATTAATTTTTCTGCTGGTGGGA
 TAAACATTAAAAATTAATCATGTTTCAAAAAAAAAA

0973194-16301

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLEKYMDEDEGEWWIAKQRGKRAITDNDM
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHENPYCPFRCSGPVCTHYTQVWVATSNRIGCAINLC
HNMNIWGQIWPKAVYLV CNYSFKGNWWGHAPYKHGRPCACPPSFGGCRENL CYKEGSDRY
YPPREEETNEIERQQSQVHDTHVTRSDSSRNEVISAQQMSQIVSCEVRLRDQCKGTT CNR
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDMPVDKRKTYIASFQNGIFSES LQNP PGKAFRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 148

GGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCAATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCGCGCTCCGACGGGCGCAGCGCCCTCCCCATGTCCCTGCTCCACGCCG
CGCCCTCCGGTCAGCATGAGGCTCCTGGCGGCGCGCTGCTCCTGCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAATGCAAGTGCTCCCGGAAGGGACCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCCTGGAACGAGAAGCGCAGGGCTACGAA
GAATAGGGGTGAAAAACCTCAGAAGGGAAGAACTCCAAACAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCCCTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACATATACATCTGAGCTTTATAAGCGCCCGGA
GGAACAATGAGCTTGGTGGACACATTTTCATTGCAGTGTGCTCCATTCCCTAGCTTGGGAAGC
TTCGCTTAGAGGTCTCGGCGCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCTCCCT
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTTCACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGAGCAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTCTTCCCTCACCACAACAGAATGCGAGTACTAAAGCAATATAT
TTGTGATTCCCCATGTAATTCTCAATGTTAAACAGTGCAGTCTCTTTTCGAAAGCTAAGAT
GACCATGCGCCCTTCTCTGTACATATACCCTTAAAGAACGCCCCCTCCACACACTGCCCCC
CAGTATATGCCGATTGTACTGCTGTGTTATATGCTATGTACATGTGAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAA

00978134-103501

FIGURE 149

MSLLPRRAPFVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

09978194.101504

FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCGGTCTGCGTCA**TGTT**AAACTCCAATGTCTCTGTG
 GTTAACTGCTCTTGCCATCAAGTTCAACCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG
 CAAATCCGGGGCCTAAGAACACCGTTACCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTTA
 TGCTTCAACCCCACTTGGAGAGAGGGCGGTTTCAAGCCCCAGAACCCCGCTCCTCTGAGCTGGCATCGGAATAC
 TACTCAGTTTGCTGTGTGTGCCCCAGCACCTGGATGAGAGATCCTTACTCTGAGTATGCTGCCCATCTGGTT
 TACCGCCAAATTTGGATACTTTTGAAGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTTAAACATCTACGT
 GCCACGGAAGATGGAGCACAACAAGAAAAACGAGATGATATAACAGAGTAAAGACCGGTGGAGAACGGAAGA
 TATTCTATGATCAAGAACAGTAAGAGCCCGTTCATGTTCTATATCTATGGGGATCTTACATGGAGGCACCGGCAA
 CATGATTGACGCGAGCATTTTGGCAAGCTACGGAACCGTATCGTGATCACCATTAACTACCGTCTGGGAATCT
 AGGGTTTAAAGTACCGGTGACCGAGGACGACAAAGGCAACTATGGGCTCTGTGAGTCAAGTCAAGACATCGCGTG
 GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC
 CTGTGTGACGCTGTTGACCTGTCCCACTACTCAGAAGGTCCTTCCAGAAGGCCATCTTTCAGAGCGGACCGG
 CCTGTCCAGCTGGGAGTGAATACCGAGCCGGCAAGTACACTCGGATATTGGCAGACAAGGTCCGGTCCAACT
 GCTGGACACCACGACATGGTAGAATGCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGCATCAACCCC
 GGCACCTTACCACATAGCTTCGGGGCGGTGATCGAGCGCGAGCTCATCCAGACGACCCCGAGTCTGTATGGA
 GCAAGGCGAGTTCTCACTACGACATCATGCTGGGCGTCAACCAAGGGAGGCGCTGAAGTTCTGTGAGCGGCAT
 CGTGGATAACGAGGACGGTGTGAGCGCCCAACGACTTTGACTTCTCCGTGTCCAACTTCGTGGACAACCTTTACGG
 CTACCTGAAGGGAAGAACACTTTGCGGGAGACTATCAAGTTTCATGTACACAGACTGGGCGGATGAAGAAAAACCC
 GGAGACCGGCGGAAAAACCTGTGGCTCTCTTTACTGACACCAAGTGGGTGGCCCCCGCGTGGCGCGGACCT
 GCAGCGCAGTACGCTCCCCACCTACTTCTATGCTCTTATCATCACTGCCCAGAGCAATGAAGCCGAGCTG
 GGCAGATTGCGCCCATGGTGTAGGTTCCCTATGCTTGGCATCCCCATGATCGGTCCCAACCGAGCTCTTCAG
 TTTGTAATTTTCCAAGAACGACGTGATGCTCAGCGCGGTGGTTCATGACCTTCAAGGCGCAATGAAGCCGAGCTG
 TGATCCAAATCAACGATTTCTCAGGATACCAAGTTTCACTTACACAAAAACCAACCGCTTTGAAGAAAGTGGCTG
 GTCCAAGTATAATCCCAAGACAGCTCTATCTGATATTGGCTTTGAAGCCAGAGTGAGAGATCACTACCGGGC
 AAGCAAAAGTGCTTTCTGGTTGGAATCGTTCTCTATTTGACAACTTTGAACGAGATATTCTCAGTATGTTTCAAC
 AACCACAAAGGTTCTTCCACAGACATGACATCATTTCCCTATGGCAACCGGCGATCTCCCGCCAGATATGGCC
 AACCACAAAGCGCAATCACTCTCGCAACAATCCCAAACTCTAAGGCACTTCAAAAAACAGGGCGCTGA
 GGACACAATGTCCTCATTTGAACCAAAAGAGATTATCCACCGAATTAAGTGTCAACATTGCGCTCGGGGCGTC
 GCTCTCTTTCTCAACATCTTAGCTTTTGGCGCGCTGACTACAAAAAGGACAAGAGGCGCATGAGACTCAGAG
 GCGCCCGAGTCCCCAGAGAAACCAACAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGAGAT
 GAAGCAGCTGGAACAAGATCACGAGTGTGAGTCTGCTGAGGCACACGACACTGAGGCTCACTGCCCCGCCAGA
 CTACACCTCAGCGCTCGCGCGGTGCGCAGATGACATCCACTTATGACGCCAAACACCATCAACATGATTCAAA
 CACACTGACGGGATGAGCGCTTTGCACACTTTTAAACACTTCAGTGGAGGACAAAAAGTACAAATTTACCCCA
 CGGACATTCACCACTAGAGTATAGCTTTGCCCTATTTCCTTCTCTATCCTCTGCCCTACCGCTCAGCAACAT
 AGAAGAGGGAAGGAAGAGAGAAGGAAGAGAGAGAGAAGAAAGTCTCCAGACAGGAATGTTTTTGTCTCCACT
 GACTTAAGACAAAAATGCAAAAGGCGAGTCACTCCATCCCGGAGACCTTATCGTTGGTGGTTTCCAGTATTAC
 AAGATCAACTTCTGACCTGTGAATGTGAGAAGTACACATTTCTGTAAAAATAAGCTTTTAAAGATCTTACCA
 CTCCAATCAATGTTTGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTGTTCCAAAGTCAATGGAAGCAGT
 GACACTTCTGAACTCAGCCAGGACACTTGATATTTTAAATTCAATGGAAGTTTAAACATTTCTTCTGTG
 CACACAATGGATGGCTCTCTTAAAGTGAAGAAAGTCAATGAGATTTTGGCCAGCACATGGAGCTGTATTCAG
 AGAAGAGAAACGTAGAAATTTATTTATTAAGAAAGTGGACTGTGACGCGAAATCTGTACGGTCTGTGCAAGAG
 GTGTTTTCAGCGCTGAATATTTTAAAGACTTTGT

0078104.101501

FIGURE 151

MLNSNVLLWLTAIAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLEPIWFTANLDTLMTYVQDQN
EDCLYLNIVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRI LADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVS NFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVYV
FGIPMIGPTLFCNFSKNDVMSAVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVP PPDMS
FFYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTELSVTIAGV
ASLLFLNILAFAALYYKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCPDYLTLRLRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 152

GGGAAAGATGCGCGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCAGGATGTTACTCCTTCTTCTTTTGTGGGGCTGGGCGAGGGCCCA
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAACCGGGAGCACTCGCTGTGCAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCTCAGTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCCTTGTGGAACCGG
GTGCCATGTTTCTTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCTCATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCCTGGTGATTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCCTGCC
CCGCGGCTACTACTTTCGGCACTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCTTTGAAGTTGTTTGAATGACAGTGGAGAGAACCCAGAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGTGTTTCTGTATTGGCA
TAGTCAATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCAGT
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACATATTTCTG
TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCTCATGGTTGTGCATGGGGACATCTAAT
CTGGTCTGGGAAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCCTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC
AGAATTTCATAGCCCAGGCTGCCGTGTTGTTTGAAGTCAAGAGGCCCTTCTACTTCAGTTTTG
AATCCACAAGAATTAATAACTGGTAACACCAAGGCTTCTGACCATCCATTGCTGGGTT
TTGCATTTGACCAACCTCTGCCTACCTGAGGAGCTTCTTTGGAACCCAGGATGGAATCT
TCTTCCCTGCCTTACCTTCCCTTCACTCCATTATTGTCTCTCTGTGTGCACTGCAGCTG
GGAAAGGCATTTTGGATGCCTCTCTGTTGGGGCTGGGGCTGCAGAACACACCTGCGCTTTCAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAATGCAGCTCCAGGTTTGATCAACCAAAAGCAACATTTGTCATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGT
TACGATTTTGGAAATCCCACTTTGAGTGTGAAAGTGAAGGAAGCTTCTTCTTACACCTT
GGGCTTTGGATATTGCCAGAGAAGAAATTTGGCTTTTCTTCTTAAGTGACAAGAGACAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCCTGGAAGAGTT
CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAATCAGGTTACAGGCCAG
AGTCTCCTTGGAGGGCTGGAACCTGAGTCTCTCTATGAACCTCTGTAGCCTTAATGAAAT
TCTTAAATCAGCGATGCAACCAAAAAAAGGCGGCGGCGACTCTAGAGTGC
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPPQVAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKEHGQGKKK
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLYDFTFLVIRYVKRHLTIMMDIDGKEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

00078314-101501

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGCGCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGGTGGGTGGTTAACTCCTCAGTGGGACTCCAGATTTCATGAAGAAAATCAGTTGTCTTTATTCAAGAAT
 TGGGGTCTGGCTCAGAAATTCCTGCAGCTGGTAAAAATCTGTTTCTAGAAAGAGTTTAATTAATGCTGCAGTCT
 GACATGTTCCCGATTTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATATGCTTTTCGCAACCGCTTCT
 TGTCTGCTGCTGGCCCTGGCTGCGTGTGCTGGCTTTGTGAGCCTCAGCCTCGAGTCTTCCACCTGATCCCGGTGT
 CGACTCTTAAGAAATGAATAGTAGCAAGATCGAAAGAGAAATCATGCCGACCCCTGTGACCGGAGCCCTGTGA
 CAGACCCCGCTTTATGAAGCTCTTTTGTACTGCAACATCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCCCC
 CGCATCATTTTAAAGCTCTCAGTGCATGTGTTTCAATTCGCCACGGAGACAGGTACCACTGATGTTTCAATCCCA
 AAACAAAGCGACAGAAATTTGATGTCACCTCTGGTGGTAAACAGGAACCGTATCACCCAAACTCTGGAAGCTTCA
 ATGTCCACATGTTCAAAAGATCCCGGAGCCTCTTCGAAAGCCCTTGAACCTCTCTGCTCTTTATCCCAATCAC
 CATTGTGTGAGATGGAGAGCTCAACACAGCAGGAGTTGTGCAGCATTTGCAGAACGCTCAGCTGCTGAGSGATA
 TCTATCTAAAGAAACAAACTCCTGCCAATGATTGGTCTGCAGACCACTCTATTTAGAGACCACTGGGAAAA
 GCGGAGCCTTCAAAAGTGGGCTGGCCTTGCTTTATGCTTTTCCCCAGATTTTGACTGGAGAGAGATTTATTTCA
 GGCAACGACCAGTGCAGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAAGAACCATGATATCTGGAAGAGGAGC
 AGCGTCTCAGTACCTCTCACTGTTGAAAAACAGCCAGCTGGAGAAAGACCTACGGGGAGATGGCCAAAGATCGTGG
 ATGTCCCAACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCATGCTCTGCCACTTCTGCCACATGTCAGCT
 TTCCCTGTACCAAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAAATTTGACTTCTGGGTATTCTCTCTGGGTGCCACCCCATCTGAAACCAACCATCG
 GCGGGATGCAGCGTGCACCGAGGGCAGGAAAGAGAGCTTTGCCCTCTACTCTGCTCATGATGTTCACTCTGT
 CACCAGTTCTCAGTGCTTTGGCCCTTTCAAGAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
 GSCAAGA CAGAGAAAGCCCAAGTGAACATTCGTCGCGATTCTTTCAATGCGGTGATGTGCATTTCAACACT
 CTTTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAACTTTGGTCCGCTTTGTGAAAA
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATATTATGATGCATGTGCACAGGGAAGGATTCTAAAGG
 TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTGTCTGTTAC
 TAAGGTTAGAAGATTATGCTTTTAAAGGCTAAATATTGTTTGGGGAACCAAGATGTTGGGGTTGAACAGT
 AAGCACATTTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAATGGCCAGTTACAGAGGAAATAGAAGGTACTT
 TATCATATGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGGCAC
 TCTTCTGGCCTGCCCATGTTACTATGTGATGGAACAGCACACCTCAACCAAAATTTTTTAACTCTAGACATT
 TTTACCTTGCTCTGTTAAGAAATTTCTGAAGTGATTATCTAAAATAAAGGTTGGCAAACTTTTTCTGTAAGG
 GCCAGATTGTAATAATTTCAAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTAACTACTCAACTCTGT
 TTTCTGAAGCAGGAAAGCCACCAAGACAGTACATAAAGGAATATGTGTAGCTGGGTCCAGGCCAGACAAAACA
 GATGGTACAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCACTAAAATAATAGGCTACTACTCAATTTGC
 ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAAATATTCAATGGTCTCTCAGTAACCTCTGATAGAAACA
 CAGAATTTGGTCTGTATCTGACACTAGAACAAACTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAAC
 AACTGATTAGAAGAATCTGATTGTTATGATGATTGTGGTACAAAGATAGTTTAAAGTATGTTCTCAATATTGTT
 CTGCTGTAGTCTATTGCTGTATATGCTGAAATTTTGTATGCCATTAGTATTTTATAGTTTAGGAAAATATT
 TTCTAAGACCGATTTTAGATGACTCTTATCTCTGTAGTATTTCAATTTGCTGTGCTGTGGTGTGAGTAGAG
 GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAAATTAGGCTTACTCCCTTTGACAGCTGTAGA
 ACTGGATTCAATTTTAAACCAATTTTATCAGTTTCAAAAGTAAATCTAGTATTGTTTAAATGCTGTTTGA
 AGAAGCTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTATATATAGAGAACCAATATATCATCTG
 TGATTTCTGAACATAATGGTGCTAATTCAGAGAATGGAAGTGAAGTGAGATTCTCTGTGTCATCCGCATCTCC
 AACTTTTCTCTTTGTTTTGTTCCAGTGTGCAATTGAATATGCTGTTTCTATAAAATAAATTTTTTAAAGATAA

0978194-101511

Figure 1. The structure of the proposed model.

Signal sequence:

amino acids 1-18

FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCTTTTGAAGAACAGTACTGTGGGA
 GCTATTTAAGAGATAAAAAAGAAATATCCTTTCTGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
 CGCGCTCTTCCACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCTTGACCGCGCTGAAGACAAAGCAGAT
 AGCTTAGGAATGAACCATCGCTGGGAGTATGTGGAACAAACGGAGGAGCTCTGACTTCCCACTGTGCCATTCTAT
 GGGCGAAGGAACTGCTCTGACTTCAAGTGTAAAGGGCAGAAATGAAAATAATTCTGGAGGAAAGATAAGAAATGAT
 TCTTGGCGCACTGCACCGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCTGGGGACTCTGTGGGAGACCGG
 ATGCAACCCAGATACGCTATTCAAGTTCGGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGAGCCT
 GGGCTGAGCTCCCGGAGGCTCGCGGAGCGCGAGTTCGCATCATCCCCAGAGTAGGACGAGCTTTTGGCCCT
 GAATCCCGCGACCGCGAGCTTGGTCAACGGCGGCGAGTAGACCGGAGGAGCTCTGATGTGGGGCCATCAAGT
 TCAATTCAATCTAGACATTCTGATGGAGGATAAAGTGAATAATATAGGATAGAACTAGAGTAAAGGACATTAA
 CGACAATGCGCTTACTTTCGTGAAAGTGAATTAGAAATAAAATAGTGAATAATGCAGCCACTGAGATCGGTT
 CCCTCTACCCCGACGCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
 CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGTGAACCGCGCCTGGACCG
 CGAAGAAAAGCGTCTCACCACCTGGTCTTACGGCTCCGACGGGGCGACCCGGTGCACACAGGCAACCGCGG
 CATCCGCGTATGGTTCTGAGTGCAGAACGACCAACCGCACCGCTTTGCTCAGCCCGAGTACCGCGCGAGCGTTCC
 GGAGAATCTGGCCTTGGCGACGAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAAGAGTCAATGCGGAAGT
 GAGGATATCCTTCGCGTATGTGGAGCACAAGCGCGCCCAAGTTTCAAACTAGATTGTAAATCAGGGACAATATC
 AACATAGGGAGTTGGAACACGAGGAGTCAAGATTCTACAGATGGAAGTGCAGCAATGGATAATGCAGGATA
 TCTCTGCGCGAGCAAAAGTCTGTATCACTGTTCTGGACGTGAACGACAATGCCCCAGAGTGGTCTCACCTCTCT
 CGCCAGCTGGTTCCCGAAAATCTCTCCAGAGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA
 GGAAAACGCAAGGTGATCTGTTTCACTCCAAAGGAAATCTGCCCTTAAATGAAAAAATCTTACGGAATTACTA
 TAGTTTAACTACAGACATAGTCTTGGATAGGGAACAGGTTCCTAGTCAACATCAGTGCACCGCCACTGACCG
 GGGAAACCCCGCCTTCCACCGGAAATCTCATATCTCGCTGAAGCTGGCAGACCAACGACAAACCCCGGCTCTT
 CCCTCAGGCTCTTATTCGCTTATATCCAGAGAACATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA
 CGACCCCGACTGTGAAGGAGAACCGCCAGATCACTTATTCCTGGCTGAGAACACATCGAAGGGCGAAGCTATC
 GTCTACGTGTCCATCACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCGCGA
 TCTCAGGTGAAGGTGATGGCGGGGACAACGGGCAACCGCCCTCAGCAGCAACGTGTGTTGAGCGTGTGCT
 GCTGGACGAGAACGACAATGCGCCCGAGATCTGTACCCCGCCCTCCCCACGAGCGTTCCACTGGCGTGGAGCT
 GGCTCCCGCTCCGAGAGCCCGGCTACCTGGTGACCAAGTGTGGCGTGGACAGAGACTCCGCGCAGAACGC
 CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGACTCTTCTCGTGGGTGTGACACAGGGCGAGGTGGC
 CAGCGCGAGCGCCTGCTGGACAGAGACGCGCTCAAGCAGAGCTCGTAGTGGCGGTCCAGGACACCGCGCAGCC
 CCCTCTCTCCGCACTGTCAACGCTCAGCGTGGCGGTGGCGCAGCAGTCCCCAAGTCTTGGCGGACTCTCGAG
 CCTCGAGTCTCCAGCTAACTCTGAACCTCAGACCTCACTCTGTAACCTGGTGGTAGCGGTGGCGCGGTCTCTCT
 CGTCTTCTGGCCTTCTGTCATCTGTGCTGGCGCTCAGGCTGGCGGCTGGCAAGTACAGCGCTGCTGAGGC
 TTCAGGAGCGGCTTGAAGAGCGCGCGCTGCACTTGTGGCGTGACCGGGTGCAGGCTTCTCTGAGAC
 CATTTCCACAGAGTTTCCCTCACCACGAGCTCGCGGAAGAGTCACTGATCTTCCCCAGCCCACTATGACAGA
 TGGAGTGCAGCGGTACGATCATAGCTCACTGGCGCTCAAACCTCAGGCTCAAGCAATTTACCCACTTTGCCCT
 CCGTGTGAACAGGAGTCAAGGTGCAAGCCACTACTGTGCTGCTATCTATCTATCTATCTATCTATCTATCTAT
 CTATCTATCTATCTATCTATCTATCTTCTGTGACAGACGGAGTCTCAGCCTGTAAATCCCGACTTTTGGGAGGC
 CGAGGGCGGTGGATCACTTGAAGGTGGGAGTTTGAAGCAGCGCTGACCAACTGGAGAAACCCGCTCTATCTAA
 AAAAAACAAAATTAGCCGGGCGGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGTG
 TGCTTTAACTGGAGGTGGAGGTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCTGGGCAACAGAGTG
 AAACCTCTATCTCA

09978194.101501

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGLTWETGCTQIRYSVPPEELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPPLPAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLLKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSCLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLQNDN
APEILYPALPTDGGSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVAVAASVCFVLAFFVILLALRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAFLQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFNCSSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLSL
IYLSIYLSIYLSIYLLSCTDGS LTPVIPVLWEAEAGGSPEVGSLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCAGTTAAAAG
GCTCCAGAATCGTGTAACAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCAATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTGTCTTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAAACCCATTGCGAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTAGGTGGCAACTGGGTCTTT
ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCCGAGAGAATTTTCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT
CTGGTTC

097534.04504

FIGURE 159

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336
<subunit 1 of 1, 260 aa, 1 stop
<MW: 28048, pI: 7.87, NX(S/T): 1
MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQQQQLLCGGVL
VGGNWWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIFVVQSIHPFCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENF PDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGD SGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY
LDWIKKIIGSKG
```

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCTGCGCGCCCCGGCCCCG
CGCGCCGCCCCAGCGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGGCCCGGGCCCGGCCCGC
GCCCGCGCCCCAGGTGAGCGCTCCGCCCGCCGCGAGGCCCGCCCCCGGCCCGCCCCCGCCCCG
CCCCGGCCCGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACTGATCCCCATAAAAC
ATTATCTCTCCCGCGGCCCGCGCTGCGAGCGCCCCCGCCAGTCCGCGCCCGCGCCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGCGGGAGC
GGAGCGCGCCGAGCCTCTGTCGCCGCGGCCGGGCCGGGGCCGAGCCGTAGCGCGCGCCTGGA
TGCGGACCCGCGCGGGGAGACGGGCGCCCCCGAACGACTTTTCAGTCCCCGACGCGC
CCCGCCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCGAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAAATGA
GCCAAGGTGACGACAAGCTGCCCCAGCAGGCGCTGCGAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCCCTGCCGAACCTACCATCTCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCTGCCACATTCCACGGCCTGGGCCCGCTACACACGCTGCACCTGGACCGC
TGCGGCCCTGCAGGAGCTGGGCCGGGGCTGTTCCGCGGCCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACCGCCTGCAAGGCACTGCCTGATGACACCTTCCCGACCTGGGCAACCTCA
CACACCTTCTCCTGACGGCAACCGCATCTCCAGCGTGGCCGAGCGCGCTTCCGTGGGCTG
CACAGCCTCGACCGTCTCCTACTGCAACAGAACCGCGTGGCCCATGTGCACCCCGCATGCCTT
CCGTGACCTTGGCCGCTCATGACACTTATCTGTTTGCCAAACATCTATCAGCGCTGCCCA
CTGAGGCCCTTGGCCCCCTGCGTGCCTGCACTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCACGCCCACTCTGGGCTGGCTGCAGAACTTCCGCGGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCTGGCTGGCCGTGACCTCAAACGCTTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCCGCGAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCCTCAGT
ACTGGAGCCTGGAAGACCACTTCCGCGAGGCAATGCGCTGAAGGGAAGCGTGGCCGCCCGGTG
ACAGCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCCTTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCGCTCACTGCAGTGGGCCCGAGGGCTCCGAGCCACCAGGGTT
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGAGCCACT
GCCGTCTGGGCCAGGCGAGCGGGGGTGGCGGGACTGGTGAATCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACTGCAGCCTCACCCCTGGGCTGGCGTGGTGTCTGGAAGTGTCT
TGGGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGTCTCAGCAGCCAGGTGTGTGTACATAC
GGGCTCTCTCCACGCGGCCAAGCCAGCCGGGCGGCCGACCCGTTGGGGCAGGCCAGGCCAG
GTCTCCTGATGGACGCTGCGGCCCGCCACCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGGCGCAGCGTTTGTTCAGAACGCGCCTCCACCCAGATGCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGAGCTGGAATAAAGAGCTCTTTTCTTAA
AAAA

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FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAAASQRI
FLHGNRISHVPAASFRA CRNLTI L W L H S N V L A R I D A A A F T G L A L L E Q L D L S D N A Q L R S V D P A
TFHGLGR LHTLHLDR CGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQN RVAVHVP HAFRDLGR LMTLYLFANNLSALPTEALAP
LRALQYLR LNDNPWVCD CRARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSEGGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGTCTCTGGAGAGGACTAC
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCCAGCCTCAGATATCTGGGACTTTAC
 AGTCCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
 AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTCCTTTCTCCTTTTGGGCTTATCTCTGGCG
 GCGCGCGGCAAGCCTAGAAGCTATTCTGTGGTGGAGGAAACTGAGGGCAGCTCCTTTGTCTAC
 CAATTTAGCAAAAGGACCTGGGTCTGGAGCAGAGGGAATTTCTCCAGCGGGGGGTTAGGGTTG
 TTTCCAGAGGGAAACAACTACATTGTCAGTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
 GAGAAATTTGGACCGTGGAGTCTGTGCGGTCAACAGAGCCCTGTGTGCTACGTTTCCAAGT
 GTTGTCTAGAGAGTCCCTTCGAGTTTCTCAAGCTGAGCTGCAAGTAAATAGACATAAACGACC
 ACTCTCCAGTATTTCTGGACAAACAAATGTGTGAAAGTATCAGAGAGCAGTCTCTCTGGG
 ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAAACAATATTGAGAACTA
 TATAATCAGCCCCAATCCTATTTTCGGGTCTCTACCCGCAAAACGAGTGATGGCAGGAAAT
 ACCCAGAGCTGGTGTCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAAAC
 CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
 CTTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGTCAGATCTCTG
 AGGACAGTCCGGTAGGCTTCTGGTTGTGAAGGTCTCTGCCAGGATGTAGACACAGGAGTC
 AACGGAGAGATTTCTTATTTCACTTTTCCAAGCTTCAGAAAGATTTGGCAAAACCTTTAAGAT
 CAATCCCTTTGACAGGAGAAATGAACTAAAAAACAACCTCGATTTGAAAACTTCAGTCTCT
 ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGAAAAATGCACCGTTCTGATT
 CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGCTCTGCATTTACAGCCCAAT
 ACTTGAGAACCGCGCTGAAACTGTGGTTGCACTTTTCAGTGTTCAGATCTTGATTACGGAG
 AAAATGGGAAAAATAGTTGTCTCCATTCAGGAGGATCTACCCCTTCTCTGAAATCCGCGGAA
 AACTTTTACCCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACACAT
 CACTATCACTGTCACTGACTTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
 TGATCGCCGATGTCAATGACAAACGCTCCCGCCTTCAACCAACCTCCTACACCCTGTCTGCTG
 CGCGAGAAACACAGCCCCGCCCTGCACATCCGCGAGCGTCAGCGCTACAGACAGAGACTCAGG
 CACCAACGCCCAGGTCACTACTCGCTGCTGCGCGCCCGAGACCCGCACCTGCCCTCACAT
 CCCTGGTCTCCATCAACGCGGACAAACGGCCACCTGTTGCGCCTCAGGTCTCTGGACTACGAG
 GCCCTGCAAGGGTTTCCAGTTCCGCGTGGGCGCTTCAGACACCGGCTCCCCGGCGCTGAGCAG
 CGAGGCGCTGGTGCAGCTGGTGGTGTGGACGCCAACGACAACTCGCCCTCTCGTGTGTACC
 CGCTGCAGAAACGGCTCCGCGCTGCACCGAGCTGGTGCCCGGGCGCGGACCGGGCTAC
 CTGGTGACCAAGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTACCA
 GCTGTCTCAAGGCCACGGAGCTCGGTCTGTTTGGCGGTGTGGGCGCAACAATGGCGAGGTGGCGCA
 CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCGCAAGCACAGCTGGTGGTCTGGTCTCAAGGAC
 AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCTGTGTGACGGCTTCTC
 CCAGCCCTACCTGCTCTCCCGGAGCGCGCCCGACCCAGGCCACGGCCGACTGTGCTACCGG
 TCTACCTGGTGGTGGCTTGGCCCTCGGTGCTTCTCGCTTCTCTCTTTTCTGGTGCTCTGTTC
 GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCTCGGTGGGTGCTGCTGTGTGGTCCCGGA
 GGGGCCCTTCTCAGGGCATCTTGTGGACATGAGCGGCAACAGGACCTATCCCAAGCTACAC
 AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTTCTGAAGCCGATT
 ATCCCCAACTTCCCTCCCAAGTGCCCTGGGAAAGAAATACAAGGAAATTTCTACCTTCCCCAA
 TAACTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTCACTTCCATAGGATTTTATT
 TGTGGCATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAAATATTGTACGGAT
 TTACTCTTGATTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
 CCTGGTTCTT

03070014-101501

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5
MEASGKLICRQQLVFSFLLLGLSLAGAAEPRSYVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSARGNKLHLQLNQETADLLNEKLDREDCGHTPECVLRFPQVLLSPFEFFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTFFLKNAEIDLVGQNNIENYIISPNSYFVLRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLVDNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATVDVTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPLMITQ
LNMVTLIADVNDNAPAFQTSTYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGLFGVWAH
NGEVTRARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPHGLVDMMSGTRT
LSQSYQYEVCLAGSGGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

03976194-101501

F **E** **D** **C** **B** **A**

ACCCACGCGTCCGCCCCACGCGTCCGCCCCACGCGTCCGCCCCACGCGTCCGCGCGTAGCCGTGC
 GCCGATTGCTCTCGGCTGGGCAATGTCCCGGTGCGCGTCGACGACCGCCCCGCGTCAT
 GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCCGTCCGCGCGTGG
 AGGTTGCAGAGGAAAGTGGTCGCTTATTGGTCAGAGGAGCAGCCTGCTCACCCCTCTCCAGGTG
 GGGGCTGTGTACCTGGGTGAGGAGGAGCTCTGTCATGACCCGATGGGCCAGGACAGGGGACG
 AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCGTG
 TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
 GGAGGAGCGGAGGACTCAAGTGCGAACGTCGAGAGAGCCTTTTCTCTTGATGGCGCTGG
 AGCACACTTCCCTGACAGAGAAGAGAGTATTACACAGAGCAGAAGTGGCGGAATCTGAG
 CAGCCCCGACAGGAGACTCCAATAAGCACTGAAAGTCTGAAATCCCCAAGGCTGAATCTGAC
 GAGAGAAACATTACAGGATTAGAAAAATTTCACTCTGAAAAATTTTAAATATGTCACAGGACCT
 TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTCTGTTTTACACCCCGTGGT
 GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
 CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
 TGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
 GAACACTGGAACACTGAAAATCTTCATTTTTTAATCAGACAGGTATAGAAGCCAAGAAGAT
 GTGGTGGTAACTCAAGCCGACCAAAATAGGCCCTCTCCAGCACTTTGATAAAAAGTGTGGA
 CTGGTTGCTGTATTTTTCCTTATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA
 CTGAGAGTATTGCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
 GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
 CATTTTCTCCGATGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAAGATCATTTTGTGAA
 CAACTGAACTGATAAAAAAATATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAAATGC
 AAAAAATATTCAATAG

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCGCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCTCTC
TTTGGCCAGCCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTC CCTTGCGCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCAC TGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCACTGTCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCGCGAGCATCCGCAAGCTGCAGTGCTTA
GTCCCCGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTGTAGAAATATTCAAACATAATA
AAATCATGAATATTTTAA

FIGURE 167

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920
><subunit 1 of 1, 295 aa, 1 stop
><MW: 33518, pI: 7.74, NX(S/T): 0
MLQGPGLLLLLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHSLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVSEKDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGELVITSVKRWQKGQREFKRISRSIRKLQC
```

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTCTGCTCGCGATC
AGCCTGTCTCAA CTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCA
TGCTGAGGACTTGGTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCTTGACTCCGTCGGGCTCCGTGCGGGC
ACCATCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCATTTGCCTTCTCATGGGTGGCCAGACCTCTGTGCCCTTGCCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCTCTGGGCGTCTTGTGGCCAATGTGCT
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGTCTCGGTGTCTATACCATCC
CTGCTGGCGTCTGCTGCTGCTGTCCACCATCTGCTGTGGGAGAGTGTGCCCCCCACCCG
CCCTCTGCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTCTCTGGCTGTGTCTTGGGGGAATGATCGGATCTCTG
CCAGCTTCTCAGCCCTCTGGAGCAGATCTCTGTGCAAGCGGCCACTCCAGTGGGTTTCC
GGCCTCTGTGGCGCTCTCTTCATCAGTTTGGGATCTCGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCTGTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCCTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA
GTGTTCTCTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGAAGTGTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCAGTCTGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGCGACTCCCGGA
GTGCACGGCGAGGGGGCCCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCGAGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCTCTTT
CTCCTCCCCGTGGGTGATCAGCTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA
TGGAGCGCAACTGGAACATCTGGTCCACCTGCGGGCGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

0378194.101501

FIGURE 169

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLIVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PPFAFLMGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSFVLV
KKGEDIPMLGLVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTTEATKIGLCFLSLACVPFALVSQQLQGQTLALAATCSLLGLFGFSVGFVAMELAVECSFPV
GEGAAATGMIFVLGQAEGILIMLMTALTVRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT
```

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCTCTGCTCAACTGGGTGAGGTCCCTCTTAGACCAGCTCTTGTCATCATTTTGCTGAAGTGGACCAAC
TAGTCTCCCACTAGGGGGTCTCCCTGGCAATCTTGATCGCGTTGGACATCTCAGATCGCTTCCAATGAAGA
TAGGCTTGCTTGCGGTCTGCTTGTTTCATAATCATCTAACTATGGGACAAGGTTGTGGCCGACGCTCTGGGG
AAGGACACCGGGCTGATCAGGCATCCAGGAAAACCTGGAGGACTGTGCCAGCTTGAAAGAACTCTAGTGGTT
TCTGAATCTAGCCCACTCTGGCGGTAAAGCAATGATGCACTCTTGCAACTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGGGATTGTGAGGAGTGACCACTCTCACGGTGAATAACCAAGTGTGAGAGGATGGC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCGGGAGGAGAGGCGAGGCAAGCTGGGGCCGCTT
CCAGGTGTTGACGCTGCTCCAGGCGCTCCCACTCAGGTGGACTCTGAGGAAGGCTTGCTCAGCAACAGGCGGG
GCTGGAATCGAGAGCAGCTGTGCCAGACAGTGGGATCCCTGCTGTTCTCTTGATGCTGTGCCACAGGGATTT
GGCTCTGATCTGATCTGGAGATCCAGGTGCTGGACATCAATGACACACGAGCCAGGTTTCCCAAGGCGAGCAGGA
GCTGGAATCTCTGAGAGCGCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCACAGACAGGCC
TAACACCTGACACCTACACTCTGTCTCCAGTGAGCACTTTGCTTGGATGTCAATGTGGGGCCCTGATGAGAC
CAACATGCGAGAATCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTGATCTGGTGTAACTGCG
CTATGACAAATGGGAACCCCCCAAGCTCAGGTACCACTCTGGTCAAGGTCAAAGCTCTGGACTCCAATGACAAATAG
CCCTGCGTTTGTGAGAGTTCACTGGCAGCTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTCTCAATAAACT
GACCGCCACAGACCTTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAATGAACACATGCTCCAGAGGT
GCTGGACAGTGTGATATTGATGCGCAAGACAGGCCAGGCTCATCTTGGCTGACCTCTAGACTATGAAAGAAACCC
TGCTACGAGGTTGGATTGTTCAGGCAAGGAGGACTGGGTCCCAATCCATCCAGGCCATGCAAAAGTCTCATCAA
GGTTCTGAGATGTCAATGACACAATCCCAAGCATCCACGTCACATGGGCTCCCGACCATCAGTGGTGTGCAAGG
TCTTCCCAAGGACAGTTTATTTGCTCTTGTCTATGGCAGATGACTTGGATCAGGACAATGTGTTGGTCCACTG
CTGGCTGAGCCAGAGCTCGGCCCACTTCAGGCTGAAAGAACTAATGGCAACACATACATGTGTGCTAACCAATG
CACACTGACAGACAGCACTGGCCCAATATACCTCACTCTGTTAGCCCAAGACAAGGAACTCAGCCGCTTATC
AGCCAAGAAACAGCTCAGCATCTCAGATCAGTGACATCAACGACATACGCTGTTTGGAGAAAGCAGGTATGA
AGTCTCCACCGGGGAAACCACTTACCTCTCTCACTCATTACCACTAAGGCTCATGATGAGACTTGGGCAAT
TATGGAAGAGGTTCTCATACCGCATCCAGGACTCCGAGTTGCTCACTTAGTAGTCTATTGATCCCAACAGAGGA
GGTCACTGCTCAGAGGTCAGTGAATATGAAGAGATGGCGGCTTTGAGTTCCAGGTGATCGCAGAGAGCGGG
GCAACCCATGTCTGATCACTCAGTGTCTCTGTGTGGGTGAGCTCTGATGAGTCCAAATGATAATGCCAGAGGTGG
CCAGCTCTGTGCTCAGCGATGGAAGAGCGACCTCTCCGTGCTTGTGAATGCTCCACAGGCCACCTGTGTTGCC
CATCAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCATGCGCCACTCAGCACTCCCGGCCATT
CCTTTTGACACCAATTTGGGCAAGAGATGCACTCTGGGGGCAATGGAGAGCCCTCTACAGCATCCGCAATGG
AAATGAAGCCCACTCTTATCTCAACCTCATACGGGGCAGCTGTTTGGTCAATGTCAACCAATGCCAGAGCT
CATTTGGGATGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTCTACAGACCCGAGCCCTGTT
GAGGGTCTATGTTTGCACCACTGTGGACCACTGAGGACCTCAGCCCGCAAGCTTGGGGCTTGAGCATGTGAT
GCTGACGCTGATCTGCTGGCTGTACTGTGAGGATCTTCCGGTTGATCTTGGCTTGTGCTGATCCATCTGCGC
GACAGAAAGAAAGGACAAACAGGGCTTACAACTGTCCGGAGGCCGAGTCCACCTACCGCCAGCAGCCAGAGGCC
CCAGAAACACATCTCAGAAGGACAGATCCACCTCGTGCTGTGCTCAGGGGTTCAGGCGAGGTGAGCCTTGTGAAGT
CGGGCAGTCCCAAAAAGTTGGACAAAGGAGGCGATGATGGAAGCAGGCTGGGACCTGCTGTCAGGCCCTT
CCACTCAGCCCGGCTTGTACAGGACGCTGCGTAATCAAGGCAACAGGAGGACCGCGGAGAGCCGAGAGTGT
GCTGCAAGACAGGCTCAACCTCTTTTCAACCATCCAGGACAGGAAATGCTTCCCGGAGAACCTGAAACCTTCC
GAGCCGCCAGCTGCCACAGGCCAGGCCAGTTCAGGCTCTGTAAGGTTGCAAGGACGCCCCACAGGAGGCTGCG
TGGAGACACAGGCGAGTGAAGAGCCCCACAGAGGCCACAGCTCTCTTCAACACTGAGACGGCAGCGACATCT
CAATGGCAAGGTGCTCCCTGAGAAAGAAATCAGGCGCCCGCTCAGATCTCTCGGAGGCTGGTCCGGCTGTCTGTGCG
TGCTCTTCCGAGGCGAACCCCTGGAGGAGCTCACTGTGATCTCTCTGATCTTCCAGTCTTCCAGTACTGCT
GTCTTGTGCTCATCAGGGCCAACTTCAGGCCAAACCAACAGCCAGGAGAAATAGTACTTGGCCAAAGCCAGGAG
GACAGGAGTGCATCCCAAGACAGATGGCCCAAGTCAAGGGTGGAGGCGCAGACAGCCAGCAAGAGGA
AGGGCTTTGGATCTTGAAGAGGACTCTCTGTGGAAGCACTCTAGAAAGAGAGCTGTCAAGTCTGTGAGGCC
AGGACAGGCTCGGCCCTGAGGACCGGCTGAGCGCCCTGACCCGGCTGATGCGAGAGCTCTTTCGCCCTCAC
CACCAACTACCGTGACAAATGTATCTTCCCGGATGCTGACGACAGGAGGACCGAGGACTTCCAGAGTTCGG
CAAGGACAGGCCACCAAGCTGAGCCCAACAGCACAGGCTGGCCAGCTTGTCTGCGAGATGAGCTCACT
CTCTGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCTGAGGCGCCCTCGAGGCGCTGCGCGGCTCTCGGT
GCTCGGAGGACCTCAGTTTAGACTTGGCCACCAAGTGCAGCTCAGGCATGAAGTGCAGAGGGAGCCAGGTTGG
AAGACCGGCACTCAGGCGCAGAGCAGAGGACGAGCAGCAGCAGCAGAGGTGCTCTGACATCATCTCAGAGCT
CTGGATCTGACAAACCAAGGCCCTGAGGATCTGTGGACAGAGCTGTTTCTAAAATCTGTGTAATCATCAGCTAG
CGCGCGCTGAGAGACTTTAGGTTGATGATGATCTACCCCAAGAGAGGACAGGCCCCAGGACTAACAGCTGAC
TGAACCAAGCAGCCCCCTGTGAGCAGCTCTGAGTCTTTTGGAGGACAGGAGCGGTTTGTGGCTGAGATAGTGT
TCTCGGCAAAACATATGTGGAGCAACAAAGGGTCAGTCTCTGGCAGACAGATGCAACGAGATACACAGGAG
AAGAGGTTGGCTTCTTGGGTGACAGGAGTCAAGGGGCTGTACCTTGGGGGTGCCAGGAAATGCTCTGACCTAT
CAATAAGGGAAGAGTAAAAAAGGAAAAAAAAAAAAA

0076197.10357

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCC GGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCACTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTTTTCATGGTGCCTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGACTGCTTTTTCTGCTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGAAACTAGGAGATCCCTTCCCATTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTCTGGATTTGGTGTGTCAACTGCCATACACTTACATGTCTTACTTCTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGG
AAGTGA AAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGTTACTTTTTCTCTATTACTGTGTTTGGGAAAATTTT
CATGGCTACCATCAATATTGTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT
TCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGATGTGTCATCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCCAATGTCATTGTCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAACTACTGAAGTCCCTGGAGAAGTGCAGTTCAACTTCTATCACCCTTGGTT
TGATGTGATCTTCTGCTGTCAGCGCTCTCTAGCATACTCTTCTCTATTGGCTCACAAAC
AGGCACCAGAGAAGCAATGGCACCTTGAACCTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACAGGGGCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTGAGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGAGAGGCCAAGAACTAA
AGGTGAAAAATACACTGGAATCTGGGGCAAGACATGCTATGTTAGCTGAGCCAAACACGT
AGGATTTCCGTTTAAAGTTTACATGGAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTATTGACAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTfMYFF
WKLGDFFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDDI
LALERLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFGWMIKSVTTSASGSENLTLIQ
QEVDALEELSRLFLETADLYATKERIEYSKTFKGKYNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIBITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTkFFYAIS
SKSSNVIVLLLAQIMGMYPVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 174

CATGGGAAGTGGAGCCGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNANACTATTTTTTGGATTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAATGAACCTGTGTGAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCAACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCCTGTCNTTATGGCTGACCTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCTATTCTC

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FIGURE 176

CTCGCGCAGGAGTCGTCCTCCATGCGCGGGGCTCGGAGCCGCGACCCTTGCGGGGGCCCTCCGGGATTGTGCTACCTTTT
TGGCTCCCTGCTCGTGCAGCTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCTTGCAGCAA
GGAGGGGCGAGGTCAGCAGCTCTTTCGGGCTTCTGTGGGCTGACACGGCAGTGTGACAGCCCGACCCAGCAGCTG
GCTGTGTTGGGTGCTTCCCGAGCCCTGGCTCTTCTGGGCGAGCAGCGGAATCGCATCTGGAGGCTCTTCTGCTGTG
CCCGTTGAGCGTGGGAGGAGCTGACTGTACAGAGTGGACATCGACCAGGAGAGCTGATATGAAAGGAAAGCAA
GGAGCAACAGTGGTTGGGAGTCAAGTGTTCGGAGCCAGGGGCTCGGGGGCAAGATTTGACTCTGTGCACCCGATGA
TGAGGCAAGGCGCAGTGGACAGCATCCTGGAGACCGGGGATATGATTGGTCGCTGTTTGTGCTCAGCCAGGA
CTTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAAGTTCTGTGAGGGGACGGCCCAAGGCCCTCAGAGCAGG
TGGGTTCTGCGACGAGGCGACAGCTGCGGCCCTTCTCCCTGATAGCCACTACCTCTCTTTGGGCGCCAGGAAAC
CTATAAATTGGAGGACACGCGCAGGCTGGAGCTTCTGTGCAGGGCTCAGCGAGGCTGGGCACACCTGGAGCAGCG
TCCCTACGAGGCGGGGGGAGAGAGGAGCAGGACCCCGCCTCATCCCGGTCCCTGCGCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGCTCTGGTGGTGCAGAGAGCTGAGCTTTTGGCTGGAGCCCCCGCGCCAACCA
CAAGGGTGTGTGTGTCATCTCGCGCAAGGACAGCGCCAGTCCGCTGGTGCCGAGGTTATGTGTCTTGGGGAGCG
CTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGG
TGCCCTTACTTCTTTGAGCGCAAGAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACAGCGGGGGCTCACTG
GGCTGGGATCCCCCTCTCGGCTCTGCGGCTCCCTGACTCAAGTTCCGGGATCAGCTGTGCTCTCTGGGGG
CTTCAACCAAGATGGGTTTCCAGATATTGACAGTGGGTGCCCTTTGATGTGTATGGGAAAGTCTTCATCTACCA
TGGGAGCAGCTGGGGTTTGCCGCAAACTTCAACAGGTCTGGAGGCGAGGCTGTGGGATCAAGAGCTTCTCGG
CTACTCCCTGTACAGGACGTCTTGATATGGATGGGAAACCAATACCTGACCTCTGTGTGGGCTCTCCGGGTGACAC
CGCAGTGTCTTTCAGGGCCAGACCCTACTCCATGTCTCCATGAGGCTCTATTGTCTCCAGAAAGCATCGACCT
GGAGCAGCCCACTCTGCTGGCGGCACTCGGTCTGTGTGAGCTCAAGGCTCTGTTTCAGTACTCAATTGACGTCCC
CAGCAGCTATAGCCCTTCTGTGGCCCTGGACTATGTGTGTAGATGGGGACACAGACCGGAGGCTCCGGGGCGAGGT
TCCCCGTGTGAGCTTCTGAGCCGCTTAACCTGGAAAGAACCCAGCAGGAGCTCCGGGCGGTGTGGTGTGAAGCA
CCAGCATGACCGAGTCTGTGGAGAGCCCATGTTCACAGTCCAGGAAATGTCAAAGCAAGCTCTCGGGCCATTGT
AGTGACCTTGTCTTACAGTCTCCAGACCCCTCGGCTCCGGGACAGGCTCTGCGCAGGGGCTGTCCAGTGGC
CCCATCTCAATGCCACAGCCAGCCAGCCAGCGGGCAGAGATCCACTTCTGAAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAAGGCAATCTGCAGCTGGTCCACGCGCGCTTCTGTACCCGGGTACGCGACACGGAATCCAAAC
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCACTGAGTGGGACAGCCAGTCAATTGGCTGGAGCTGAT
GGTCACCAACCTGCCATCGGACCCAGCCAGCCCAAGGCTGATGGGGATGATGCCATGAAGCCAGCTCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGCTCGGGCCCTGGACCCTGCGGAGAGGCCACTCTGGCTGTCCAA
TGAGAATGCTCCCATGTGTGATGTGAGCTGGGGAAACCCATGAAGAGAGGTGCCAGGTCACTTCTACTCAT
CCTTAGCAGCTCCGGGATCAGCATTTGAGACCAAGGAACCTGGAGGTGAGAGTGTGTGTGGCCAGATCAGTGAGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCGTGTCTTATTGAGCTGCCACTGTCCATTGCGAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTGTGTGGTGGGGGGCAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCGAGCAAGGT
CAAGTATGAGGTCAACGTTTCCAAACCAAGGCCAGTCTGCTCAGAACCCCTGGGCTCTGCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTATCCCAATGACAGGTTGAGCTGAGGGCGGGCAGGGGCTGG
TGAGAAGAGGAGTGTCTCCAGGCCCAACATCTTCCACTGGATGTGGACGATAGGGATAGGAGGCGCGGGA
GCTGGAGCCACTGAGCAGCAGGAGGCTGTGTGAGCGGCGAGGAGCCAGCATGTCTGTGGTGGCGAGTGTCTCTG
TGAGAAGAAGAAAAACATCAGCTGGACTGCGCCCGGGGACGGCCAACTGTGTGGTTTTCAGTCCGCACTTCA
CAGCTTTGACCGCGCGGCTGTGCTGATGTCTGGGCGGCTCTGTGAAGACAGCCTTCTTGGAGGATGACTCAGC
TGTGAAGTCTCTGGAAGTGAATTTCTCCGGGCCAACATCAGAGTCAAGTGAAGTCTTGAAGAAGTGTGATCTCCAGA
TGCCTCCACAGTGATCCAGTGAATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAGGAGTGCCTGTGTGGT
CATCTCTGGCTGTGATGCTGTGGGCTGTGGTGTGATGACCTGTGGTGTCTGTGTTGAGGAATGGGATCTTCT
CAACGGGGGAGGACCCCGAGGCGACCGTGCAGGATACCATGCGGTGAAGATTTCTCGGGAAGAACGACAGCA
GTTCAAGGAGGAGAGACGGGCACTCCTGAGGAAACACTGGGGCAGCCCGGGGAGGCGGCCGATGCACA
CCCCATCTGGCTGTGACGGGCACTCCGAGCTGGGCCCCGATGGGATCCAGGGCCAGGCAACCGCTAGGTTCC
CATGTCCAGCTGGCTGTGGCTGTGGCTCCATCTCTCCAGAGATGGCTCTTGGGATGAAGGGGTAGAGT
GGGCTGCTGGTGTGCAATCAAGATTGGCAGGATCGGCTTCTCAGGGGACAGACCTCTCCACCCAGCAAGAAC
TCTCTCCACCAACTCTCCCTTAGAGTCTGTGAGATGAGAGTGGTAAATCAGGACAGGGCGATGGGTAGGG
TGAGAACGGCAGGGGTCTCTGATGCAAGAGTGGGAGAGGGATCTTAATCTCTCTCTCTCTCCATCACTCTGT
GTAACAGACCCCAAGACACTGCTCTCCCGGAAGTGCTTAACCTAGAGGCTCGGGGAGGAGTGTGTGCTACTGA
CTCAGGCTGCTCTTCTAGTTTCTCCCTCTCATCTGACCTTAGTTTGTGCACTCAGTGTAGTGGTTTCTGTGGT

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FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQANRTGGFLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGGPKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGWKFCEG
RPQGHQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGSTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRILIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSFGFYS LAVADLNSD GWPDLIVGAPYFFERQEELGGAVVYVYL NQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLNDGFPDIAVGAPFDGDKVFIYHGSSLG VVAKPSQVLE
GEAVGIKSPGYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDA DTRRLRGQVPRVTFLSRNLEEK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAI VVTLSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPS TQRABIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTALFA
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGNPMKRG AQVTFYLILSTSGIS IETTELEV ELLLATIS EQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGSRLTIGSAFLNIM
WPHEIANGKWLLYPMQVELEGGQGPQKGLCS PRPNILHLVDSDRDRRRRELEPPEQQEPEGE
RQEPSMSWNPVSSAEKKKNITLDCARGTANC VVFSCLYSPDRAAVLVHWGRLWNSTFLEEY
SAVKSLEIVIRANITVKSRIKNLMLRDASTV I PVMVILDPMAVVAEGVPWVVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHFEATVPQYH AVKIPREDRQQFKEEKTGTILRNNWGS PRREGP
DAHPILAADGHPELGDPGHGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGTGGCT
CACAAACAAGATGCCTCAAGGTGTGAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTTCGACGGCGGTAATTTTC
TGGATGATAAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGAAC
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCAGCCCTGTTTGTGGTTTCAGATGGTCATACCTACTCTTTTCAGTGC
AACTAGAATATCAGGCATGTGTCTTAGGAAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCTCTTCAGATAAGCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAACAGATTGCGGGACTGGTTCAGGCGCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCTGAGAGAAGCAGATTCGATACCAGCATC
TTGCCAATTTCGAAGGACTCACTTGGCTGGATGTTTAAAGACTTGATACAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTTCTCAATTCTTGTGACACATACAAGGACAGTTTAAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCTATGGCAGTGTGGACAGTGTGGTGTGTGACAGATATGGAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGACAGATTGTGCTATAGATTTTGAGATCTCCGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGAGTGGTGGTATGAC
CATGATGTATACATTGATGATGACAGTTGAAATCAATAAATTTACATTTCTAATATTTTA
CAAAAATGATAGCCTATTTAAAAATTATCTTCTTCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTGTATAATTATTTGAAAAATTGACAGCTAAAGTTATAGAAGTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCTTACACAAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAGTTTTGAGTGCTACTATAATAAATTTTTCACGAGAACAAAATTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG
ATAATTCTAAGTGAAATTTAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAA

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FIGURE 179

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAVAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPCVVYPSFVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLLRPERSRFDTSILPI
CKDSLGMFMFRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDEGYKPTQCHGSVGGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI
```

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

0978194.10504

FIGURE 180

CAGACTCCAGATTTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGACGGAGAGACAACAGTACCTGACGC
 CTCITTCAGCCCGGGATCGCCACAGCAGGGGATGGGCGACAAGATCTGGCTGCCCTTCCCGCTGCTCCTTCTGGCC
 GCTCTGCCCTCCGGTGTCTGCTGCTGGGGCGGGCGGCTTACACCTTCCCTCGATAGCGACTTCACTTTACCCCTT
 CCCGCGCGCAGAAAGGAGTGCTTCTACAGGCCCATGCCCTGAAGGCTCGCTGGAGATCGAGTACCAAGTTTAA
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAGGCAAAACCTTAGTTTGAACAAAGAAAA
 TCAGATTGAGTTACACTGTAGAGCTGAAGTTGGTGATTACATGTTCTGCTTGACAAATACATTCAGACCAATT
 TCTGAGAGAGGTATTTCTTTGAATTAATCTGGATTAATATGGGAGAACAGGCACAGAACAAGAGATTGGAAG
 AATAATATTACTGGCAGAGATATATTGGATATGAAACTGGGAAGACATCTCGGAATCCATCAACAGCATCAAGTCC
 AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACAGCATCAAGAAAGC
 AACTTTGATAGAGTCAATTTCTGCTCTATGGTTAATTAGTGGTCAATGGTGGTGCAGCCATTCAAGTTTAT
 ATGCTGAAGAGTCTGTTGAAGATAAGAGAAAGTAGAACTTAAACTCCAACTAGAGTACGTAAACATTGAAA
 AATGAGGCATAAAAATGCAATAAATCTTTACAGTCAAGACCATTAAATGGTCTTCCAAATATTTTGAATATA
 AAAGTAGGAAACAGGTATATAATTTAATGTGAAAATTAAGTCTTCACTTCTGTGACAGTAATCTGCTGATCCAG
 TTGTACTTAAGTGTGTAACAGGAATATTTTGAGAAATATAGGTTAACTGAATGAAGCATATTAATAACTGCAT
 TTCTCTAACTTTGAAAATTTTGCAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCAATTTGCAACCC
 AGTCTGTTTTAAACAGGTTCTATTACCAGAACTTTTGTAAATCGCGCAGTTACAAATTAACCTGTGGAAGTTT
 TCAGTTTCTAAGTATAATAACTCACTGAGAAATACCTAATGATGATTAATAAATCTTTAGACTACAAAAGCCAA
 CTTTTCTATTATTAACATGACATCTCTCCTATAATGTAATAGAAATCTTTAGACTACAAAAGCCAA
 AGATTTTGAACCAATACATTTCACTGATAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
 CAAAAGCTGACATTTTCAAGATTCTTAAAAACACAAAGTTACACTTACATAAATTAGGACATGTTTCTCTTTG
 AAATGAAGATATAGTTTAAAAGCTTCTCCTCCATAGGGACACATTTCTCTAACCTTAACTAAGGTAGGA
 TTTTAAATTAAGGTGAGGTAAAAATAGTTTATTTTAAATAGTATCTGCAAGTTAATATCTGTCAACAGTTAA
 TAATCATGTTATGTTAATTTAAGCATGATTGCTGACTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA
 TTGCTAAAATGATCTGGGCTACCATAAATAATATCTCTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA
 AGAATTTAGAAAAAATGAGAAAACTTAATCCAAATAAAATTCACCTTAAGTAGAATATAAATAAATATCTAGA
 ATCTGACTGGCTCATCATGACATCTTACTATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
 AAACCTTGGCTGAGGTTTTTATTTCTACAAGAAATCTGGTTGAAATTTTGTGAAGCAGGTACATTTTATA
 AAATGTAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATAAAAATTTTATATAACAACTTTTAT
 TAAAAATGGCCTTCTGAACACTTTATTTATGATGTTGAAGTAAGGATAGAAACATAGACTCCCAAGTTTTAAA
 CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGCTTAC
 TCAAGTACTAGTAATTTAACTTCAATGAATGAACATAAATTTTAAAGTTATGCCATTTATAAGCTGTGTTAT
 GACTACATTTGTGAGTTAGAAACAAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT
 CTTGATGAGCAATAATGATAACCCAGAGAGTGATTTCAATTACACTCATAGTAGATAAAAAGAGATACATTTCCC
 TCTTAGGCCCTCGGGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTAAAAATGAGGTAAGTAAATGCCGTAT
 ATGATCAATTAACCTTAATTGGCCAGAGAAATGCTTCAGGTGCTAGGGGTATCTGCAACACTTGCAGAACAA
 AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGGCCTGTTAAATTTGCAATGAGAAGCAATTTACA
 TAGCCATAACTAATAAGCAGGGTACAGATATAAACTACTGCATCTTTCTATAAACTGTGATTAAGAAATCTTA
 CCTCTCCTGTATGGCTGTACTGTACTGTACTCTCTGACTCTTACCAATCAATGAATTTGTATACATAATCTCT
 ACATGTATGATTTTGTGCCAGATCTTAAACCTATGATTCAGTAATCTTTACCTATAAAAACGATTAATGCTT
 TATTTGAAAAAGAAATTTAGGAATACTAAGGCAATATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
 CATAACCAAAAAGCAAAACTTGTAAACAGAGTAAAAATCTTAAATTTTAAAGACATACCTGTTTATCTGCTT
 CATATGCTTTTAAATTTCACTATTCATTTCTAAATTAAGGTTATGTAATGAGTAAGCTGTTTATCTACATT
 AACAGCTCATTTTGTCTTTTCAATATACAAATTTAAAAATACTACAATTTAACTAAGGCCCAACCGGATTC
 CATATATGTGACAGTACCGTGTCACCTCACACTAAGGCTAGAGTTGCTCTGATATGCAATTTGGATGTAAT
 GTTATGCTGTCTTCACTGTAATGTCAAGACATGGAGGCTGTTGTAATTTTATGGTAAATTAATCTCTTA
 CACATAATGTTGCTTAAAAATGACAAAAATGAGCACTTCAATTTGATGCTCTCTCAATGAAGATCTTTTAT
 GTGAAATTTAAAGACATGATTCGCATGTAAGGATTTTCACTGCAATCAATATGCAATCACTGAGTTG
 CTCAACTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTTATTTGGTACTGATGATATTAATAA
 AAATATCAAAGGAAAA

00978194.101501

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLPPFVLLLAALPPVLLPGAAGFTPSLSDSDFFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDPHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTPSTISEKVIFFEL
ILDNMGEQAQEEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRRKSR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

0978194-30350

FIGURE 182

CCATCCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGCTCCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAGTGC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCC
TTCTTTTCTTTTCTTACCTTCATTTCAGGCTTTTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

09978104.104501

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965
<subunit 1 of 1, 175 aa, 1 stop
<MW: 19330, pI: 7.25, NX(S/T): 1
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGABGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPIVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

05978194-701501

FIGURE 184

CCAGTCTGTGCGCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCA**ATG**CGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTCTGGC
TGCTTGC GGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTAACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGT**AG**AGTCCCCGCCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAA

CG928104.101501

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

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FIGURE 186

CTGCAGTCAAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCGCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCAATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCGCGGGAGGGGACGCGAGCGGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCAAGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACTTGTGCAG
GACACTAAACAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG
TGATTGCAGTAAATTACTGTATTGTAAAATCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTATCTTGACTGACAAATATTCTATATTGAACCTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAGCATAACCCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTGGAATGACAAATGATAGGTACCTAAAAATGAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTGA
AATAAAATTTAACATTTAAAAA

THE BIBLE

<subunit 1 of 1, 266 aa, 1 stop

MMALGAAGATRVFVAIVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGTLYPGGNKYQTDINDYQPPYCAEDEECGTDBEYCASPTRGGDAGVQICLACRKKRRKCMRH
AMCCPGNYCKNGKICVSSDQNHFRGEIETITESFGNDHSTLDGYSRRTTLSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKBEQVCTKHKRKGSHGLEIFQRCYCEGLSCRIQ
KDHHEANSSSRLHETCORH

Signal peptide:

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAAAG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

105107-4618260

FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCGGTGTGGCTGCACCTCACCACATCCCGTGGCGCGCGG
 CTGGGCGGTGCGAGAGTGCCTGTGCTTTCTCCTGCAACGCGGTGCTTGGGCTCGGCCAGGCGGGTCCGCGCGCA
 GGGTTTGAAGATGGGGGATAGCTACAGGAAGCGACCCCGGATGGCAAGGTATATTTTGGGAATGAAAAGGA
 AGTATTGAAATGAGCTGAAGACCATTCACAGATTAAATTTTGGGGACAGATTGGTGATGCTGATTCACCTT
 TGAAGTAACTGACACAGAGTTCTCAAAATTTGCATATTACATCAACTGGAAACACAGCTGAATCTTAAATGTTTAC
 TTAATCAGAATTTGCATAAGAAAAGAAATGGGAGTCTGGTTAAATAAAGATGACATATCAGAGACTGAAAAG
 GATCATTTCTGTGTTTTCTGTAGTGTATATGGCCATTTTAGTGGGACAGATCAGGATTTTACAGTTTACTTGG
 AGTGTCCAAAACCTGAAGCAGTACAGAAATAAGACAAGCTTTCAAGAAATTTGGCATTGGAAGTTACATCCTGATAA
 AAACCCGAATAACCCAAATGACATGGCGATTTTTAAAAATAAATAGAGCATATGAAGTACTCAAGAGTGAAGA
 TCTACGGAATAAGTACAAATGAGGAAAGGGAAGTGGAGATATCAAGGTGGCCAGTGAAGCTGGAA
 CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATACATTTGGAAGAAGAGAATTTGATGC
 TGCTGTAAATCTGGAGAACTGTGTTTGTAAATTTTACTCCCAGGCTGTTACACATCCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTCGAATTTGAGCTGTAACTGTGGTGATGATAGAA
 GCTTTGCGGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTCGGTCTGGAATGGCCCGATGAAATA
 TCAATGGAGACAGATCAAGAGGAGATTTAGTGAGTTTGCATGCGAGCATGTAGAAGTACAGTGACAGAACTTTG
 GACAGGAATTTTGTCAACTCATACAACCTCTTTTGTGCTGGTATTTGGCTGGCTGATCACTTTTGTTCAAA
 AGGAGAGATGTTTGTACTTCACAGACAGACTCAGGCTTAGTGCCATGTTGTTTCTCAACTCATTTGGATGCTAA
 AGAATATATTTGGAAGTAAATCACTAATCTTCCAGATTTTGAAGTACTTTTCGCGCAACACACTAGAGGATCGTT
 GGCTCATCATCGTGGCTGTATTTTCTTATTTTGAAGAAATGAAATCAATGATCTGAGCTGAAATACT
 AAAAATCTACTTAAAAATGATCATATTCAGTTGGCAGGTTTGAATGTTCTCTGCAACAGACATCTGTAGTAA
 TCTGTATGTTTTTCCGCGCTCTCATCAGTATTTTAAAGGACAAAGAACCAAGAAATGAAATTCATCATGAAA
 GAAGATCTCATATGATATCTTGCCCTTGGCAAGAAAGTGTGAATTTCTCATGTTTACACAGCTTGGACCTCAAAA
 TTTTCTGCCAATGCAAGAAACACTGGCTGTTGATTTCTTTGCCCTGGTGTCCACATGTGGCGCTTACT
 ACCAGAGTTACGAAGAGCTCAAAATCTTCTTTATGGTCAAGTTTAAAGTTTGGTACACTAGATGTACAGTTTATGA
 GGGACTCTGTAACTGATATACTTTAGGCTTATCCAAACAACAGTGGTATTCACACGCTGCAACATTCATGATGA
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
 ACCCAACCTCTCAACGAATAGTTTACAAAGAAACACAAACGAAGTCTGGATGGTGTATTTCTATTCTCCGTG
 GTGTCATCCTTGGCAAGTCTTAAATGCCAGAAATGAAAGAAATGGCCCGGACATTAATCTGAGCTGATCAACGTGGG
 CAGTATAGATTTGCCAACAGTATCACTTTTGTGCGCCAGGAAACGTTCAAGATACCTCTGAGATAAGATTTT
 TCCCCCAAAATCAAAATAAGCTTATCAGTATCAGAGTTACAATGGTTGGAATAGGAGTGTCTATTCCCTGAGAT
 CTGGGCTCAGGATTTTACTCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCAAGTAAAGTCTTCAAGG
 GAAAAATCATTGGGTGATTTGATTTCTATGCTCCTTGGTGTGGACCTTGCAGAAATTTTGTCCAGAAATTTGAGCT
 CTGGCTAGGATGATTAAGGAAAGTGAAGCTGGAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGCGCTATCCAATCTGTTAAGTTTATTTCTACGAAGAGCAAGAGAAATTTTCAAGAAGAGCA
 GATAAATACAGAGATGCAAAAGCAATCGCTGCTTAAATAGTGAAAAATTTGGAACCTCTCCGAATCAAGGCCAA
 GAGGAATAAGGATGAATTTGATAATGTTGAAGATGAAGAAAGGTTTAAAGAAATTTTCAGACAGATGACATCAG
 AAGACACCTATTAGAAATGTCAATTTATGATGGGAATGAATGAACATTTCTAGACTTGCATTTGATCTGCCA
 GAATTTCTCAGACACTGGTGTAAGAAAGGGGCTGCAAACTTTTCTGTAAGAGGCGGGTTTATAAATATTTTA
 GACTTTTTCAGGCTATAAATGTTGCTTCCACATGAGAAACAAGATAGACTCATGTATTCTTTGTTTATTTGCT
 TTTAACAACTTTTAAAAAATATTAAGCATTTTACTGCTCAGAGCCATCAAAAGTAGGGCTGGATTCAGTCCATG
 GACCATGATGCTGTTCCCTCTCGACGGACTTAAATGTTTTCAGTGGCTGGCTGGAACATGAGCTGCTGTGCT
 ATCTACATAAATGTCTAGTTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAGAGGTAACT
 TAGTTTTTGGTCACTTTGTTTCTTAAAAATGCTATCCCTAACCATATATTATTTTGTTTTTAAAAACCCAT
 GATGTGGCACAAGTAAACAAACCTGTTATGCTGTTATTTATGATGAGGAGATTTCTCATTTGTTTCTTCTCTCA
 AAGGTTGAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACGTCAGCATGATTTGTGCACATGAGTAACTACA
 AAATTTGAGCAACAGTAAGTGCACAAATTTCTAGTTTTCGTTATCATCTCAGGAAAACTTGAGGAAAAAATTA
 TAGCAATTAACTGCGCAATGTAGAGTATCTTAAATATGTTATCAAGTATTTAGAGCTCTATATTTTAAAGATATA
 TGTGTTCTATGTTTTCGAAATTTGCTTTCTAGAAATTTCCCACTGATAGTTGATTTTGTAGGCACTCAATAT
 TTAATATTTTGCCTCTGAACTTTGTTTGTGACCTGTATCCTTTATTTACATTTGGGTTTCTTTCTTCTAGTTTGG
 TTTTTCACCTCTGCTCAGTCTTTATTTATTTCAATAGGAAAAATTACTTACAGGTTGTTTTCATGTAGCTTAT
 AATGATCTCTGATTTTATCCAGTTACTAGTTTACTGTCAGAGGGCTGCCCTTTCAGTAAATTTAGACATAAT
 ACTGAAGTTATTTTATAGAAAAATCAAGTATATAAATCTAGGAAGGGATCTTTCAGTTTCTGTGTTTGTAGA
 CTTCAAGAAAGTCAAAATTTTGCAGTAACTGATGTTGTTAGTTATTAATTCAGAGTTGCAGAGATGTAAATAT
 CCAATCAGTCAAAAGAGGTCAAAGATTAAGGCTTGAACCTTTTCAAAAAAATAAATAA

09978104-303501

090314 101000Z

Important features:

amino acids 744-747

amino acids 158-163

amino acids 77-96

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAG
GTCGTTGGTGAAAGTTTTTCATTCCCTCAGAGGAGAAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGCGCTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCTAGGACATTTTTGGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCCTT
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTACCA
AAAATCCAAGCACAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAGCTTTATTTTACATTTTT
TCAGTCTTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAGATTA
ATTACCTGTCTTCTCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGCTGTTTTTCTCT
TCATGCCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTTCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCAAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCTCTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCTCTATATTTCTCTCCCTTTTTATAGTCTTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCTTGGTCCCAGAGATGTTTAGACAAAT
TTTAGGCTCAAAAATTAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

0978104-10163

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTFYFAKRQSI
LVLWDINKRGVEETAACRKLGVTAHAYVVDSCSNREBIYRSLNQVKEVGDTVIVVNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTASVCGHEGIPYLIPYC
SSKFAAVGVFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSRID
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

097844-104504

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGG
ATGCCCCGGCTCTGCAAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACGTCCTTCT
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCGGGGCCGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCAGCCGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCAGCA
CGTGACAAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCGTGCGGACCC
TTCGTGCGCCTGATCTCCGCTTCCGCGAGCAAGTTGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCCCGGTGCCCATGCTGCGGCTGTACGCCAACACACAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACCGCGCG
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAAGCTTTCGCGTTCGCTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

FIGURE 194

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4
MTKARLFRLWLVLGSVFMILLIIIVYWDSAGAAHFYLTSTFSRPHTGPPLPTPGPDRDRELT
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESEVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLLRGAFYRDLRIPIREHVHNASAHLTFNKFWRRYGLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELNEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLQLQLQVDRQLRFPPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD
```

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

00978794-33534

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 162. **Figure 154**
 163. **Figure 155**
 164. **Figure 156**
 165. **Figure 157**
 166. **Figure 158**
 167. **Figure 159**
 168. **Figure 160**
 169. **Figure 161**
 170. **Figure 162**
 171. **Figure 163**
 172. **Figure 164**
 173. **Figure 165**
 174. **Figure 166**
 175. **Figure 167**
 176. **Figure 168**
 177. **Figure 169**
 178. **Figure 170**
 179. **Figure 171**
 180. **Figure 172**
 181. **Figure 173**
 182. **Figure 174**
 183. **Figure 175**
 184. **Figure 176**
 185. **Figure 177**
 186. **Figure 178**
 187. **Figure 179**
 188. **Figure 180**
 189. **Figure 181**
 190. **Figure 182**
 191. **Figure 183**
 192. **Figure 184**
 193. **Figure 185**
 194. **Figure 186**
 195. **Figure 187**
 196. **Figure 188**
 197. **Figure 189**
 198. **Figure 190**
 199. **Figure 191**
 200. **Figure 192**
 201. **Figure 193**
 202. **Figure 194**
 203. **Figure 195**
 204. **Figure 196**
 205. **Figure 197**
 206. **Figure 198**
 207. **Figure 199**
 208. **Figure 200**
 209. **Figure 201**
 210. **Figure 202**
 211. **Figure 203**
 212. **Figure 204**
 213. **Figure 205**
 214. **Figure 206**
 215. **Figure 207**
 216. **Figure 208**
 217. **Figure 209**

TCTGGGCCAGAATTCTGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACCGCCT
ATGCCGGGAAGGTGGTGGTCTGTACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGC
GCCTTCGTGAACAGCGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCTTGTTTCTGAGACCATCCGCCGATTGTGGCCGCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA
AGAGTCAAGGGAATGTATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCTTAGGGCCACAATCCGAGAGGGCATGCTGGCCCG
CCACTGGGCCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTCGCCCTCCGA
AGCCAACCTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGACCCCGTGAGACGCCCCGATATCCCTTCTGTAATTTCTCTCATT
CTACTTGGGGCCCCCTTCTTAGGACTCTCCACCCCAAACTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTCTGCAGCC

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPFQRPETSAQGFRQLLELNLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

09978194-101501

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAAACCTG
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC
GTATCCCCGTGGACCTGCCGAGGCACGGTGCCGTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGTGTTTCAGCCAGGTTCTGTGCGCCGCCG
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAACACTGACTTTTGAAA
GCAAG

10076194-103504

FIGURE 198

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294
<subunit 1 of 1, 180 aa, 1 stop
<MW: 20437, pI: 9.58, NX(S/T): 1
MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEYY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL
GCVNPFMTQEDRSMVSVFVSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF
```

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCTTCTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGCGCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCGAGGAGGCGCGCTGCCGCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCTCCAACTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCATGGTGTCTCATCTGCCAGCAGACTGATTGAGAAATGGGAGGCTTTTGCAGAA
TGGTGAATACTTTCAGATCAGTGTGGGAAGGTAGATGTCATTCAAGAACAGGTTTGTAGTG
GCCGCTTCTTTGTCAACACTCTCCAGCATTTTTTTCATGCAAAAGGATGGGATATTCGCCGCT
TATCGTGGCCAGGAATCTTCAAGACCTGCAGAAATATATCTTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTTCACAACTATTTTACAGTGACTCTTGGAAAT
CCTGCTTGGTGTTCTTATGTGTTTTCTGTCATAGCCACCTTGGTTTTTGGCCCTTTTATGGG
TCTGGTCTTGGTGGTAAATATCAGAAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAAATGAAGAAGAAAACAAAGCAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAAGCCAAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCCTGCCCAGC
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGTGACAAGGGAC
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAACTCTTAATTTTTCTGAAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACAGAGGAGGCCATTCCAGTCTCAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCTCTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATGTCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCTCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCACCATGGGCATTGAGGCTCT
CCACACTCTTCACTATTATCTTGTGTGAGGAGCTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTCTTACTTGAACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT
TTACAAGACAGATTAATAAAAAAATGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAGAGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCTATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAAATACTAAAAAACCACTTCTGATTTTCTTTCAGTGATGTGCTTTTGGTGA
GAATTAATGAACCTCCAGTACTGAAAGTGAAAGATTTGATTTTGTTCATCTCTGTAATC
TTCCAAAGAAATATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

00978304.101504

FIGURE 200

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433
<subunit 1 of 1, 349 aa, 1 stop
<MW: 38952, pI: 4.34, NX(S/T): 1
MAGGRCGPQLTALLAAWIAA VAATAGPEEAALPPEQSRVQPM TASNWTLVMEGEWMLKFYAP
WCPSCQQT DSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYILEKKWQSV EPLTGWKSPASLTMSGMAGLFSISGKIWLH LNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVIS ECFYVPLPRHLSE RSEQNR RSEEAHRAEQLQDAE EEEK
DDSN EEEKNDSLVDDEEEKEDLGDEDEAE EEEEEEDNLAAGVDEERSEANDQGPPGEDGVIRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL
```

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 201

ATCTGGTTGAACTACTTAAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
 TGACTCAGAGATTCTCTTTTGTGCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
 CAAATGCTATATCTATTACAGGGGCTCTCAAGAACAAATGGAATATCATCTCGATTAGAAAAAT
 TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
 TGTTTTCAGAGAAAGGATCGTGTGCTGCATCTCTCTTGGCGCCTCATTGCTCTAATTTTGG
 GAATCCATATGCTTTGGTAATATCGTGTATAGCTGTGGTCCTGGGTACCATGGGGGTCTTTTCC
 AGCCCTTGTCCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTACAGCATGTCACT
 AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCACTGGGCTCTAATCTCCTAAAGATAG
 ACAGCTCAAAATGAATTTGGGATTTATAGTAAAAAAGTGTCTTCCCAACCTGATAATTCATT
 TGGATAGGCTTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
 CTCTTCTAACTTATTTTCAGATCAGAACCCAGCTACCCAGAAAAACCATCTCCAAATTTGTG
 TATGGATTACCGTGTCACTATTATGACCACTGTGTAGTGTGCGCTCATATAGTATTTGTG
 GAGAAGAAGTTTCAATGTAAAGGAGAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
 AGGAGGACAGAAAAACAGAACAGAAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAAATG
 TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATGAAGGGAGAGGGCTGTGATTTCT
 GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG
 AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTATTATTATTTTTTGAGATAGGGCTCT
 CACTTGTATACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
 CTCAGCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATTGCCAGGCTAATTTTTTGGTG
 TTTTTTGTAGAGACTGGGTTTTGCCCATGTTGACCAAGCTGGTCTCTAACTCTCTGGGCTTAAG
 TGATCTGCCCCCTTGGCCTCCCAAAGTGTCTGGGATTACAGATGTGAGGCCACCAACCTTGGC
 CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTTACCTTGGGTAAGCCATAAGCGA
 ATCTTAATTTCTGGCTCTATCAGAGTTGTTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
 GTGTTGCCACGATTTGACCCCTCAACTCTAGCAGTATATCAGTTATGAATGAGGGTGAAT
 ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
 ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
 CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
 TTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGCGCAGGCTGGAGTGCAACGG
 CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCCTCAGCCT
 CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTAGT
 AGAGACAGGGTTTCTCCATGTCTGGTCAAGGTAGTCCGAACTCTGACCTCAAGTGATCTGC
 CTGCCCTCGGCCTCCCAAGTGTGGGATTACAGGCGTGAGCCATGCACCCAGGCTAGAATCT
 TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTCTGCTTTTTTAAATACA
 AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTTATGGA
 ACAAGTATTAACTTTTGGAAATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
 ACCATTTTTTTCAGTAATTACTGTAAAAATGGTATTATTGGGAATGAAACTATATTTCTCATG
 TGCTGATTGTCTTATTTTTTTCATACTTCCCACTGGTGCTATTTTTTATTTCCAAATGGATA
 TTTCTGTATTACTAGGAGGCATTACAGTCCTCTAATGTTGATTAAATATGTGAAAAGAAAT
 GTACCAATTTTCTAAATATGCAGTTTAAATGGATGATTTTTATGTTATGTGGATTTCAT
 TTCAATAAAAAAACTCTTATCAAAAAA

09978194-101561

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAAPPWRLIAVILGILCLVILVIAV
VLGTMGVLSPPCPNWIIEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

[illegible][illegible]

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7
MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFC SQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAAH PASRSFPDPRGLYHFC LYWNRHAGRLHLLYGKRD FLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWSPQNISLPSAASFTFSFHSPPHTAAHNASVDMCELKRD LQLL
SQFLKHPQKASRRPSAAPASQQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETV RRE
TQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGC VVSALACLV TIAAYLC SRVPLPC
RRKPRDYTIKVH MNLLAVFLDTSFLLSEPVALTGSEAGCRSAIFLHFSLLTCLSWMGLE
GYNLYRLVVEVF GTYVPGYLLKLSAMGWGFPIFLVT LVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVS YITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVL TLLGLSLVLG
LPWALIFFSFASGT FQLVVLVLYLSIITSFQGFLIFWIWYSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

03976640-10504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCCTTTCCTGGATGGGCCTCGAGGGG
TACAACTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTCCTGTTCAACATGG

CCCTGGCTGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGTTCAGGTCACGGTTTTCGCTTGA
 TCCTTTTCAAAAACCTGGAGACACAAGAAGGGCTCTAGGAAAAAGTTTGGATGGGATTATGTGGAAATCACTCC
 CGGATTCTCTGCTGCCAGACAGCGCTCGGGCGCTTCCACCCGAGTCAGACCTTCCCTTGGCGGTGTGTGAAAGAGAC
 TCGGGAGTGCCTGCTTCCAAAGTGGCCCGCTGAGTGAGCTCTCACCCAGTCAGCGCAAATGAGCCCTTCTCGGGC
 TTCTCTGCTGACATCTGCCCTGGCCCGCCAGAGACAGGGGACTCAGGGCGGAATCCAACCTGAGTAGTAAATTC
 AGTTTTCAGACAACAGGAACAGAACGGAGTACAAGATCCCTCAGCATGAGAGAAATTAATTAATCTGTGCTACTAATG
 GAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
 AGGAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGT
 ATGATTTTGTAGAAGTTGAGGAACCAATGATGGAATATATAGGGCGCTGGTGTGGTCTTGGTACTGTACCAG
 GAAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTCCCTCTGCAACCAAGGT
 TCTGCATCCACTACAACATTGTCTATGCCACAATTACAGAGAGCTGTGAGTCCTTCACTGCTACCCCTTCAGCTT
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTTAGTACCTTGAAGAAGCCTTATTCGATATCTTGAACCA
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAA
 GAAAAATCCAGAGTGGTGGATCTGAACCTTCAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCT
 CAGTGTCCATAAGGGAAGAATCAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTCCTGGTTAAACGCTGTG
 GTGGAACTGTGCTGTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
 ACGAGGTCCCTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTACCCGACGTGGCCCTGGAGC
 ACCATGAGGAGTGTGACTGTGTGTCAGAGGAGCAACAGGAGGATAGCCGCATCACCCAGCAGCTCTTGGCCCA
 GAGCTGTGCAAGTGCAGTGGCTGATTCTATTAGAGAACGTAATGCGTTATCTCCACTCTTAATCTCAGTTGTGCT
 TCAAGGACCTTTCATCTTTCAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAAGAGTTGTGCA
 AACGCTCTTTTGAGAGGAGGCTTAAGGACAGGAGAAAAAGGTCTTCAACTGTGGAAAGAAAAATTAAGATTTGTAT
 TAATAGATCACGAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTTC
 GATACGCTCTCCGCTTAATGTGTCAGTACAGGAAAAAACTGTGCAAGTGAGCAGCTGATTCCGTTGCCTTGCTTAAC
 TCTAAAGCTCCATGTCTGGGCCATAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTGCTCATATTTCAT
 ATGTAAACAGACAACATTCTATGTACTACAACCTGTTTTTAAAGGAACTATGTGTGCTATGAATTAACATTGT
 GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGGCCATTAGAAGAGAGAACTACA
 TTCATGTTTGAAGAGATAAACCTGAAAAAGAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
 TTTCAATGTGTACATTTTATATCTCCTTTTGACATTATAACTGTGGCTTTTCTAATCTTGTAAATATATCT
 ATTTTTTACCAAAGGATTTTATATCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCT
 AAACACAATTTGTATAGCCAGAGGAAACAAAGATGATATAAAATATTTGTCTCTGACAAAAATACATGTATTTC
 TTCTCGTATGGTGCTAGAGTTAGATTAACTGTCATTTTAAAAAACTGAAATGGAATAGAAATGGTAAGTTGCAAA
 GACTTTTGAATAATTAATAATTATCATATCTCCATTCTGTTATTTGGAGATGAAAAATAAAGCAACTTATGA
 AAGTAGACATTTCAGATCCAGCCATTACTAACCTATTCCCTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
 AAAGCACTTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAAACATCTTATTTA
 TTGTGATGTGTGGTTTTATTTATCTTAAACTCTGTTCCATACACTTGATATAAATACATGGATATTTTTATGTACA
 GAAGTATGTCTCTTAACAGTTCATTTATGTCTCTGCGCAATTTAAAGAAAAATCAGTAAAAATTTTTGCTGTG
 AAAATGCTTAATATNGCTAGGTTATGTGGTGACTATTGAAATCAAAATGTATTGAAATCATCAATAAAGGA
 ATGTGCTCTATTTGGGGAGAAAAATTAATAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAAATGCGGCC

09978104.101501

FIGURE 207

MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

Signal sequence:

amino acids 1-14

09978494-304504

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACTCTCATGCTCTGCTCTCTTCAACGAGACCTCTACATTCCATTTTGAAGA
AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTTCTATCCTTTTAACTAATCCTAATTTCC
AACTCCTTCTGGGGCTAGATGGTTTCTTAAAACCTCTGCCCTGTGATGTCACTCTGGATGTCTCAAAGAACCATGTG
ATCGTGGACTGCACAGACAGCATTTGACAGAAATTCCTGGAGGTATTCCCAAGAACCCAGAACCTCACCTCT
ACCAATTAAACCACTACAGACACATCTCCCCAGCGTCTTTTACAGACTGGACCATCTGGTAGAGATCGATTTAGAG
TGCAACTGTGTACTATTTCCATCTGGGTCAAAAAACACACTGTGCGATCAAGAGGCTGCAGATTTAAACCCAGAAAGC
TTTAGTGGACTCACTTATTTAAAATCCCTTTACCTGGATGGAAACCCAGCTACTAGAGATACCCGAGGGCCTCCGC
CCTAGCTTACAGCTTCTCAGCTCTTGAGGCCAACCAACTCTTTCCATCAGAAAGAGAACTCAACAGAACTGGCC
AACTAGAAATCTACTCTAGCTGGGCCAAAACCTGTATTATCGAAATCCTTGTATGTTTCATATTCAATAGAGAA
GATGCTCTCTTAACTTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAACTGCACAGCGCTCCCTACTGT
TTGCCATCTACTTTAAACAGAACTATATCTCTCAACAAACATGATTGCAAAAATCCAGAAGATGATTTTAATAAC
CTCAACCAATTAACAATTTCTTGACCTAAGTGGAATTCGCCCTGTGTGTTATAATGCCCAATTTCTCTGTGGCGC
TGTAATAAATAATTTCTCCCTACAGATCCCTGTAATGCTTTTGATGCGCTGACAGAAATTAAGAGTTTACGTCTTA
CACAGTAACCTCTCTCAGCATGTGCCCCCAAGATGGTTTAAAGAACATCAACAACTCAGGAACCTGGATCTGTCC
CAAAACTCTCTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCGAGCCTCATCCAATTTGGATCTG
TCITTCAAATTTGAACCTCTCAGGTCACTATCGTGATCTATGAATCTATCAAGCATTTTCTTCACTGAAAAGCCTG
AAAATTTCTCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACTCTCGCCATTCAATAATCTTCAA
AATCTTGAAGTTCTTGATCTTGGCACTAATCTTATAAAAAATTTGCTAACCTCAGCATGTTTAAACAAATTTAAAGA
CTGAAAGCTAGATCTTTCACTGAATAAAAAATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGTCTCAAT
GCCAGAACTCTCTAGAAAAGTTATGAACCCAGGCTCTGGAACAATTAATTTATTTAGATATGATAAGTATGCA
AGGAGTTGCAGATTCAAAAAACAAAGAGCTTCTTTCTATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCGAGCC
TTGGATCTAAGTAAAAATAGTATATTTTGTGCAAGTCTCTGATTTTTCAGCATCTTCTCTTCTCAAAATGCGCT
AATCTCTCAGGAATCTCATTTAGCCAACTCTTAAATGGCAGTGAATTCACCACTTTAGCAGAGCTGAGATATTTG
GACTTCTCCAACCAACCGGCTGTATTTACTCCATTCACAGCATTTGAAGAGCTTCAACAACTGGAAGTTCTGGAT
ATAAGCAGTAAATAGCCATTAATTTCAATCAGAAGGAATTAATCATATGCTAAACTTTACCAAGAACTCAAAGGCT
CTGCAGAACTGATGATGAACGACAAATGACATCTCTCTCCCTACAGCAGGACCATGGAGAGTGAGTCTCTTAGA
ACTCTGGAATTCAGAGGAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACCTTACAATTTATCAAG
AATCTGCTAAAAATAGAGGAATTAGACATCTCAAAAAATCCCTAAGTTCTTGGCTCTGCGAGTTTTGTATGAT
ATGCTCCAAATCTAAAGAACTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
CTAAAGAACCTGGAACCTTTGGACCTCAGCCACCAACCACTGACCACTGTCCCTGAGAGATTATCCAATCTGTCC
AGAAGCTCAAGAACTCTGATTTCTAAGAAATAATCAAATCAGGAGTCTGACGAAGATTTTCTACAAGATGCTTC
CAGTTGCGATATCTGGATCTCAGCTCAAAATAAAATCCAGATGATCCAAAGACAGCTTCCAGAAAAATGTCCTC
AACAACTGGAAGATGTTGCTTTTTCATCATAATCGGTTTCTGTGCACTGTGATGCTGTGTGGTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACAAGGGC
CAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTCTTCTCACTTTCCATA
TCTGTATCTCTCTTCTCATTGTGTGATGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT
TTCTGTAAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACAGACTGTTGCTATGATCTTTTATTGTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAGAGAGAAA
CATTTTAAITTTATGTCTCGAGGAAAGGGATCGTTACAGGGCAGCCAGTTCTGGAACCTTTCCAGAGGATA
CAGCTTAGCAAAAGACAGTGTGTTGTGATGACAGACAGTATGCAAGAGCTGAAATTTTAAAGATAGCATTTTAC
TTGTCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTGATATTTCTTGAAGAGCCCTTTCAAGAG
TCCAGTCTCTCAGCTCCGGAAGAGGCTCTGTGGAGTTCTGTCTTGAATGGCCAAACCCCGCAGCTCAC
CCATCTCTCGGAGTGTCTGAAGAACGCCCTGTGGCCACAGACATCTGTGGCCCTAGTCAGGTGTTCAAGAA
ACGGTCTAGCCCTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCTGGC

FIGURE 209

MVFFPMWTLKRQILILFNIIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTTNNLTLTINHIPDISPASFHRDLHVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLEYLDGNQLEIPQGLPPSLQLLSLEANNIFSIKKNLTTELANIEILYLGQNCYR
NPCYVVSYSIEKDAFLNLTCLKVLSLKDNNTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDSLQNFLAKEIGDAKFLHFLPSLIQLDLFSNFELQVYRASMNLSQAFSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVKNIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEBELHKEVLDDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTRTMESES
LRTLFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSCLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHRFLCTCDAVWFVWWVNHTEVTIP
YLATDVTVCVGPAGHKQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE
RDWLPGQPVLENLSQSISQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSFLQLRKLRCGSSVLEWPTNPQAHPHYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACACAGAAACATGCGAAAAACATGTTCTCTTC
AGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTCCTGTGAGTTATGCGCCGGAAGAAAAATTTTCTA
GAAGCTATCTCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCGAGAGTGCAGCAATCGTGCATCAGAGAA
TTCGCCAAACGGTGGGCAAAATATGTGACAGAACTAGACCTGTCTGATAAATTTCAATCACACACATAACGAATGAAT
CATTTCAAGGGCTGCAAAAATCTCACTAAAAATAATCTAAACCAACAACCCCAATGTACAGCACAGACGGAATCT
COGGTATACAAATCAATGGCTTTGAATATCACAGAGCGGGCAATTCCTCAACCTAAAGAACTTAAGGGAGTTACTGCT
TTGAAGACCAACAGTTACCCCAAAATCCCTCTGTTTGGCCAGAGTCTTTGACAGACATAGTCTAAATTCAAAACA
ATATATACAAATACATAAGCTAAAGAGGGCAATTCAGAGCTATTAATACTTGAAAAATCTCTATTTTGGCCTCGAATGCT
ATTTTAAACAAATTTGCGAGAAAACTAACATAGAAGATGGAGTATTTGAAGACCGTGCACAAATTTGGAGTGTCTAT
CACTATCTTTCAAGTCTCTTTTCAACGTGCCACCAAACTGCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA
CCGAGATCAAATCATTAGTAGAAGAGATTTCAAGGGATGTGATAAATTTAACTATTACTAGATTAAAGCGGGAAT
GTCCGAGGTGCTTCAATGCCCAATTTCCATGCGTGCTTGTGATGGTGTGCTTCAAATTAATATAGATCGTTTGT
CTTTTCAAACCTTTGACCCCAATTCGATACCTAAACCTCTCTAGCACITTCCTCAGGAAGATTAATGCTGCTGCT
TTAAAAATATGCTCATCTGAAGGTGCTGGATCTTGAATTCAACTATTAGTGGGAGAAATAGTCTCTGCGGGCAT
TTTTAACGATGCTGCCCGCTTAGAAATACTTGAATCTGCTTTTAACTATATAAAGGGGAGTTATCCACAGCAT
TTAATATTTCCAGAAACTCTCTAAACTTTGTGCTCTACGGGCATTGCAATTAAGAGTTATGTGTTCCAGAA
TCAGAGAAGATGATTTCCAGCCCTGATGACGCTTCCAAACTTATGCATCTCAACTTGGGTATTAATTTTATTA
ACCAATCGATTTTCAAACCTTTCCAAATTTCTCCAATCTGSAATATTACTTGTGCAAGAACAGAAATCAC
CGTGTGTAAGATACCCGGCAGAGTTATGCAAAATGTTCTCTTTCAACGTCTATTCGGAACGACGCTCAA
CAGATTTTGAGTTGTACCCCAATCGAAATCTTTATCAATTTCAACCCGCTCTTTATAAAGCCCAAAATGTGCTGCT
ATGAAAAGCGCTTAGATTAAAGCTCCAACAGTATTTCTTTTATTGGGCCAAACAAATTTGAAATCTTCTCTGACA
TTGCTGTTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAATGAAATTTTCAGCCATTTCTCATG
TCAAAATATTTGGATTTGACAAACATAGACTAGACTTTGATAATGTAGTGCTTACTGACTTTGCGCACTGG
AAGTCTAGATCTCAGCTATATTTACACATATTTTCAAGATACAGCGGTAAACACTCATATGAAATTTATTCAAA
ATTTTCAAAATCTTAAAGTATTTTAAACTTGAGCCACACAACTTTTACTTTTAAACAGATAGTATAACCTCGGAAA
GCAAGTCCCTGTAGAATATAGTTTTCAGTGGCAATCGCCTTGACATTTTGTGAATGTGATGACACAGCAATGTA
TCTCCATTTCTGAGAGTCTCAGAAATCTGACAGCTTGGATTTATCCCTTTATAGGTGTGAAGCAATCCCAATG
AAGCATTCCTTAATTTGCCCGCAGTCTCACTGAACATCATATAAATGATAATATGTTTAAAGTTTTAACTGGA
CATTTACCCAGCAGTTTCTCTGCTCGAGTTGCTTGACTTACGTGGAACAAACTACTCTTTTAACTGATAGCC
TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCCACTCACTCTGCTGCTTCT
TTTCTGAAGTCAGTAGTCTGAAGCACTCGATTTAAGTTCRAATCTGCTAAAAACAATCAACAAATCCGCACTG
AAACTAAGACCAACCAAAATTTATCTATGTTGAACTACACGGAACCCCTTTGAATGCATCTGTGACATTTGAG
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTCAGAGCTGTAGATGTGCTTTGCGCACTCCTG
GGGATCAAAGGGAAGATGATTTGTGAGTCTGGAGCTAAACACTTGTGTTTCAGATGTCACTGCAGTGATATTA
TTTTCTTCAGTTCCTTTTACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTTGTTTATCTGGGATGTT
GGTTTATATAATGTTGTGTTTAGCTAAGGTAAAAGGCTACAGGCTCTTTTCCACATCCCAAACTTTCTATGATG
CTTACATTTCTTATGACCAAAAGATGCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCCACTTGAAG
AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGAGAGAGGATTTGGGACCCGGGATTTGCCATCATCGACAACC
TCATGCGAGACTCAACCAAGAGGAAAAACAGTATTTGTTTAAACAAAAAATATGCAAAAGCTGGAACTTTA
AAACAGCTTTTACTTGGCTTTGACAGGCTAATGGATGAGAACATGGATGTGATATATATTATCTGCTGGAGC
CAGTGTTCAGCATCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCTCCAGCTGGCCTGACA
ACCCGAAGGCGAGAGGCTGTTTGTGGCAACTGAGAAATGTGCTTGACTGAAAATGATTCAGGTTATAACA
ATATGTCAGATTGCAATTCATTAAGCTACTTAACTAGTCATGATTTGCGCCATATAAAGATGCAAAAG
GAATGACATTTCTGATTTAGTATCTTATTTGCTATGTAACAAATATCCCAAACTAGTGGTTTAAACCAACACA
TTTGTGCGCCACAGTTTGTAGGCTCAGGAGTCCAGGCCAGCATAACTGGTCTGCTGACAGGTTCTCAG
AGGCTGCAATGAGTGTTCACAGAGACATAGGCATCACTGGGCTCACTCATGTGGTTGTTTCTGATATCA
ATTTCTCTGGGCTTATGGCCAAAGCTCATCTCATGTAAGCATGCGAGCTCTCCCAAGAGGAGCTGCTCT
ATCAGAGCTAGCAAAAAAGAGAGTTGCTAGCAAGATGAAGTCACAACTTTTGTGAATCGAATCAAAAAAGTAT
ATCTCATCTTGTGCGCATTTCTTATTTTGTAGAAGTAACACACAGTCCACCAAGCTCCATCGGAGTGCACAC
TCAGTCCAGGAAAAACAGCTGAAGACCAAGATGGTGGCTGATTGCTTCAAGTGGTCAATGAAATTTTCCCT
TGACTGCTGCTGGGATGGCTGCTATCTTGTAGTAGATTTGTGAATATCAGGAGGAGGAGGATCACTGTGGAGC
ATCTTAGAGTGAACCTAACACATCTCTTTTCAATATCAAGAACTTTTGGCATTGACATGAGCAATGCTCAATG
TTAAGCTGTGTTTATATTTATCATATATCTATGGCTACATGGTTATATATTGCTGTGGTTGGCTTCGGTTTAT
TTAAGTGTGTTTATAAATATTTGCTGTAACTTTGACTTCAAGTTTATAGTGCATTTAAGAACTGAGATGAG
ATAGCTTTTAAAGCATCTTTTACTTCTTACCAATTTTAAAAAGTATGACGCTAAATCTGAAGCTTTTGGTCTATA
TTGTTTAAATGGCAATTCGTGTAAATCTTAAATGAATGAATAAATGTTTCATTTTCAAAAAAATAAAAAA

09978194-103501

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGNLNITDGAFNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFSLNTQIKYISEEDFKGLINL
TLDDLSGNCPRCFNAPFPCVPCDGGASINIDRFQNLTLQRLYNLSSTSLRKINAAWFKNM
PHLKVLDFEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQPLNLSTINLGINFIKQIDFKLFQNFSLNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLTLSSHNRISHLPSGFLSEVSSLKHLDLS
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITIMVMLAALAHHLFYWDVWFYINVLAKVK
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID
NMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTEENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGD PVSES FVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

03978104.101501

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCAACGGGGGCCCGGGAGGGGAACCTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCACCAACCGGAGGAGCAGCTCTGCCCCGTGCCGGGGATGACTGATTCT
TCCTCGCCAGGCCACCCAGAGGAGAAGGCCACCCGCTTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGTGTGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCGTAGGGTGTGTGTGTCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTG
TGCAGCGTGTGTACCAGCCCTTCTCACCACTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCTACCGCCGAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGTGCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACCGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCATGAAGGAAGAAGTGCAGAGGTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGAGCCTCTGGTGCACCTCTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTTGGAGGAGCAGCTGGGGTCTGCTCTGCAAGAAAGA
CTCGTGACTGCCCCAGCGCTCCAGGCTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGTCCAGAAGCCACCTCGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCTCTTCTTCTTCTTCTTCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCAACCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAAATAAAATGAAACGTG

0978194.10501

0363-9760

Signal sequence:

1-19

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGG
CCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGACGCTCCTGGTGCATCC
TTCAGCAGCTCGGCCCATCGACTCCCTGAGCGAGCAGATTTCCTTCTTGAGGAGCAGCT
GGGGTCTCTCTCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGTGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTCTTCTCCTCCCCCTTCTCGGGAG
GCTCCCCAGACCTTGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGG
CCTCAGTGGGGCTGTGCCTGACCCCCAGCACAATAAAAATGAAACGTG

09078144.101561

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRIQSRVDLLEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQIG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

09978194.301591

FIGURE 218

GGTGGCCACAGCTGGTTTATGGGCCCCGACCCTGGGGCCCCCTTGTTCAGGAGGAGACAGCCTCCCGGCCCGGGAG
 GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCTGGGACGGTCCGTTTCTGCCTGTCAGCTGCCGCCG
 AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGTGTCTCCCTTCTCCGCTGGGCGGTATTATCGGGAGG
 AGATTGGCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGCAGGAATAGCAGGCCAACGTGAT
 TCAAAAGCTGGGCTCAGCCTCTGTTTCTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA
TGCTCTGTGATGGTGGTGAGAAAGAGGTGACACGGAAATGGGAGAACTCCAGGCAGGAACAACCTTTTGTGTG
 ATGGCCGCTCATGATGGCCCGGCAAAAGGGCATTTCCTACCTGACCTTTTCTCATCCTGGGGACATGTACAC
 TCTTCTTCGCCCTTTGAGTGCCGCTACCTGGCTGTTTTCAGCTGTCTCCTGCCATCCCTGTATTTGGTGCCATGCTCT
 TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCTGGAGTGATTCCTCGGGCGCTACCCAGATG
 AAGCAGCTTTCTAGAAATGGAGATAGAAGCTACCAATGGTGGGTGCCCGGGGCCAGCGACACCGCTCGTA
 TCAAGAAATTTCCAGATAAAACACAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCGGGCTCCCC
 GGGCTCCCATGTGAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCATGCCCCGGGTGGGGAATTGTG
 TTGGAAGAGGAACCTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCTCACATCTATGTCTTCGCT
 TCAACATCGTCTATGTGGCCCTCAAATCTTGAAATTTGGCTTCTTGAGACATTGAAAGAACTCTGGAACGT
 TTTCTAGAAGTCTCATTTGCTCTTTTACACTCTGGTCCGCTGGGACGTAGTGGATTTCTACTTTCTCTGCT
 CTCTCAACAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAAATCGGCTCAGAATCCCTACAGCC
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTCTGTGTGCCCTTGGCCCCAGATGTGCTGATCGAAGGGTA
 TTTTGCCACTGGAGAAAGTGAAGTGCACCTCCAGTACTCAAGAGACAGTAGCAGCTCTTGCCACAGAGCC
 CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGAGGACAGCAGCACTCCCGAAGAGATGCCACTCCAG
 AGCCCCCAGAGCCACACAGGAGGCGAGCTGAAGCTGAGAAGTTAGCCATATCATGGAAGAGACTTTTGTGTGT
 TAATTTGGCTATGAGAGATTTTCAGGTGAGAAGTTAAACCTGAGACAGAGCAAGTAAGCTGTCCCTTTTAACT
 GTTTTTCTTTGGTCTTTAGTCAACCAGTTGCACACTGGCATTTCCTGTCTCAAGCTTTTAAATTTCTGAACT
 CAAGGCAGTGGCAGAAGATGTCACTCACCTCTGATAACTGGAATAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
 CCAATGGCTCAGCCACAGGGTCCCCCTGGACCCCTCTCTCCCTCAGATCCAGCCCTCTGCTTTGGGTAC
 TGGTCTCATTCTGGGGCTAAAGTTTGTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACTGTGAGTCCAGA
 GGCAGTCAAGAGACCTCTGGCCAGGGGATCTTAAGTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
 TGGGGTCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTTGCCCAAAATCCTTTTAGGAATGGGACAGGTACCT
 TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGTTTTCTTTTGTACTCTGTCTCCATTAGGAG
 CAGGAATGGCAGTAATAAAGTCTGCACCTTGTGTATTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC
 ACTATCCCTCAGACTCCCTGTGTGAGCCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
 GCTCTCTCTCTCTCTCTCCCCGATGTACCTTCAAATAAAAAAAAAAATGCTAACAGTTCTTCCATTAAAGCT
 CGGCTGAGTGAGGGAAGCCAGCACTGTGCCCTCTCGGGTAACCTCAAGGCTTCGGCCCACTCTGTGCT
 ATGGTAACCACTGGGGGCTCTTCCAAAGCCCCGCTCTTCCAGCACTTCCACCGGAGAGTCCACAGGCCATGT
 CACCCTGGGGTGGGCTGTGGCCCCAGTCAGCTCTGTCTCAGGACCTGCTCTATTTTCAGGGAAGAGATTTATGT
 ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTCTCTTTTCAAGCAGGGTCTGTCTGTGATGACTTAT
 CGGCTGGGGAGGTGAACCGGAACCTTTCTATTTTGAAGCGATTAAACTGTGTCTAATGCA

09978194-101501

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCDDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGNCV GKRNYRYFYL
FILSLSLTTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLCFFTLWSVVGLTG FHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCCCTGTATTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGAATTGTGTTGGAAAGAGGAATA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

FIGURE 221

GTGTGTCTCTCAGCAAAACAGTGGATTAAATCTCCTTGACACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCCTCAGTGCACATATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAGATTTC
TTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTGAGGCATCACC CGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGAAAAACAGACCTTTCCTCTCAAACTCATCTTTCAATGTCTCTG
AACATGACTATGGAACTACACTTGCCTGGCCCTCAAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGCGCCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTGAAGTGTAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTAAAAAAGAAATTGAA
AATTGCCTTGAGATATTTAGGTACAATGGAGTTTCTTTTCCCAACGGGAAGAACACAGC
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGAACCTCTTTGGTGCCAGTGTGGGCCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGTGC GG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGTQCEASAV
PSAEFQWYKDDKRLIEGKKGVKENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKKF

Signal peptide:

amino acids 1-28

097814-30150

FIGURE 223

GAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

059744.10151

FIGURE 224

ATGGCTGTGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCGACTCCACC**ATG**GAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCTCAG
AAGGGGACAGACAGCTGTTAGGCTCACGCACGACGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACACAGAGACCCATCCACAGCACCTGCCCTTACA
GAGGCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
CAGTTCTCTGTGGGGGTGGATTTCGGAGGAAACCCCTGCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACAGGCCATCTACTGAAGCACCTGCTTGAAAAACACCACTTCAACTCTCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCTACAGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCAATGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACTTACGGGGCCCTGGGACAGGACAACTTTATGGAGTGTGTGAAG
GCAGTAGCAGGGACCTTACAGGGCCACCCCACTTCTTACCGCTACATCAGTGCAGCTCTAAGAGTTCCAAACAGC
AATGTATCTCAGGTGGACAGTCTGGGCTCTTTCTGCGCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCTTATCTGGATTACATGGAGGAACCTGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCAGAGTGCCTCAGGACAGCGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGGCGCCCTCATGGACTGGCTTTGAGTTC
CTGCTTTCTTGTGTGTACCAATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACCGCAGGAAACCAAGCATCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACTCAAGCCTGGACCGACGCTTTGAGTCTGCAACAGAGAGCTGCTGGAGACCTCTATGSCACTAAGAAG
TCTGTGTGCGGAGGTGGCAGACCTGCATCTCCAAACAGGATGACGCCCTTGGCTTTGCTTTGGGTCACCTTTC
GTGAAGGCCACGTTTGACCGGCAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCAATTTGAG
GAGGCCCTGGCAGCAGCTGTTTGGATGGATGAGAAGACCCCGCAGGCAGCCAGGAGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCCAAGCTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAAAATGTTGAATTGTACAACTCTCTGCAAGGTATTGGCTGACCACTCCGCAAG
CTTCCAGCCGAGACCAAGTGGAGCATGACCCCCAGACAGTGAATGCTACTACTTCCAACTAAGAATGAGATC
GTCTTCCCCGCTGGCATCTCTGACGGCCCCCTTCTATGCCCGCAACACCCCAAGGCCCTGAACTTCGGTGGCATC
GGTGTGGTCACTGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCAGATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAAATGAGTCCCTGGCAGCCTTCCGGAAACCAACCGGCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGAGAAACATTACTGACAACGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCACTGCCAGCGTGGGGCTCACCC
AACCACAGCTCTTCTTCTGGGATTTGCCAGGTGTGGTGTCTCGTCCGACACAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCAACTCCCGTGACTCTCTGGCGG
CACTTCCGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGT**TAG**ACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCTGACAAAGCTGTTGTCTCTTGGTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGCTTAGTCCCTCCCCCAACAGGTGACATGAGTACAGACCCCTCTCAATCACCACATTG
TGCTCTGCTTTGGGGGTGCCCTGCTCCAGCAGAGCCCCACCACTTCACTGTCGATCATTTTCCGTGTCACTCT
GCTTGAAGAGTGTGGTGGGAGCCAGTTCCTCATAGGAAGGAGTCC

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FIGURE 225

MNVALQELGAGSNVGFQKGRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQ NQA
ILKHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVL TAY
LDYMEELGMLLGGRPTSTREMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLETLYGTTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFEERALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRLVGLTLSNSRDLRLHFGCPVGSPMNPGLCEVW

Type II Transmembrane domain:

amino acids 32-57

FIGURE 226

GCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCGCGCTCCGCGGCCCTCCTCCCTCCCTCCCTCC
 CAGCTGTCCCGTTCCGCGTCATGCCAGAGCTCCCGGCCCGCCGCGCCCGCTGTCTGCTCCCTGGGCTGTCTGTCT
 CGGCTCCCGGCCCGGCCCGGCCCGCCGCGCCAGAGCCCGCCGCTGTCTGCCATCCGTTCTCAGAGAGGAGCGCTGCC
 CTTCCGGGGAGCGCAGGTAGGTGGGCGCCCGGGGAGGCGCGCGGGGAGTCCGCTCGGGCGAGCTCAGCGC
 CAGCCCGGAGGGGCGCGGGGCGCAGGTGTCTCGGCGCGCGCGCGGCCCGGAGGGTGGGCGGGGGCAGAGAGGGC
 GCGGTCTGTGGGACCCCGGACCCGCGGCGAGCCCCCGGGCGGCA CAGCGCGAGCTGGGCGAGCGGCTCCAGC
 CAAAGCCGCTCCCGCGAGGCTGCACCTTCGGCGGGAGAGTCTATGCTTTGGACGAGAGCTGGCACCCGGACCTTAGG
 GAGGCCATTTCGGGTTGATCGCTGTGCTGTGCGCTCGAGGCGCAGTGGGCTTCGCGTACAGGGGCCCTGG
 CAGGCTCAGCTCCAGAAACATCAACACAGAGTGCACCAACCCCGGCTGTGGGCGAGCCGCGCAGCTGCCGGGAC
 CTGTGCGACAGCTTCGCCCCAGGACTTCGTGGCGCTGTGTACAGGCGGAGGTCCGAGCGGCTGGACAGGCGCG
 AGTCTCGCTGTGCGCTCAGGCTCCGCTTCTCTATCTCTACAGGCGGCTGGACCGCCCTACAGGATCCGCTT
 CTCAGACTCCAATGGCAGTGTCTGTTTGGACACCTTCAGCGCCCGACCCCAAGATGGCTGGTCTGTGGGCTGTG
 GCGGGCAGTGCCTCGGTTGTCTCTCGGCTCCTTAGGGCAGAACAGTGCATGTGGCACTTGTGACACTACTCA
 CCCTTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGTCCCGAGAGACTTCAGTGCCGCTGTGAC
 TCTAGAAGGCCCCACAGCAGGGCGTAGGGGGCATCACTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA
 TTTTGTGCTGCTTCGAGGGCTTCAGGACTAACCCAGGTTCCCTTGAAGCTCCAGATTCAGACAGGGGCA
 GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCAGGAACAGGCTTTGCTGAGGTGCTGCCAACTGACAGT
 CCAGGAGATGGATGGCTGGTGGTGGGGAGCTGACAGTGGCTGGAGTGGGCGAGGCTAGCGGCTGGCAGT
 CAGTGACACTGCTGCTGCCAGGAAGAGCTGCCAGCTCTCTGCAAAGTGTCTTTTGGGGCTAATGGCTGATGCC
 AGTCCAAAGCGGTGCTCGCGCTCAGCCAGGCTCACTCTGCTAGGAAATGGCNCCTGATCTCCCGAGTCAATTT
 GGTAGGACACAGCTGAGGTGGTGGCCATGACA CTGGAACCAAGGCTCAGCGGAGGGATCAGCGGCTGCTGCT
 GTGCCACTGCT
 TCATATGCTGCTGTCAGAAATGAGCTCTTCCTGAACTGGGGCAGCAAGGACTTCGCGCGGAGGATCAGCGGCT
 GTAGGCT
 CCCTGTGTAAGAGCCAAAGCAGCAGGCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 GCT
 TGCGGCGCTGCTGAGAGGATCTATGCTGCTCAGAGGCCAGGGGTGTGGTGAAGGCGCGCGGGCGAGAGGCTGTGCG
 GCACCTGGCAAAGGCAATGGCTTCCTGATGATACCAACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCT
 CTCTCCAGGTGCA CATAAGCAACCAATGTGAGGTGTGGCGAGCTGCGCTGGAGGCGCGCGGGCGAGGGGCT
 GCGGCGCTGGGGCTCCGGATACAGCTCTCTGCTGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 CAAACCTGTGCTGCTGCTGCGGCGCGCCGAGACCCCAACACATGCTCTTCGAGGGGCGAGCAGCGCCCCACCGGGC
 TCGCTGGGCGCCAACTACAGCCCGCTGTGCTCACTCTGCACTGCGAGAGCAAGCGGTGATCTGTGACCCGGT
 GGTGTGCCCACCGCCAGCTGCCACACCCGCTGAGGCTCCGACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT
 TTTGATGTGACCGGAGCTGGCGGGCAGCGGTCACCGGTGCGACCCCGTTGTCGCCCTTTGCTGCTTAATTA
 GTGTGCTGCTGTCTCACTGTCAAGCAGCGGGGCACTGGAGAGGTGCACTGTGAGAAGTGTGAGTGTCCCGGCTGGC
 CTGTGCCAGGCTGTGCTGCTCAACCCCAAGCACTGTGTCAAACAGTGTCCAGGTGAGAGCCACCCAGCTGGG
 GGAACCCATGCGAGGTGATGGGCGCGGGGCTGCCGCTTTGCTGGGCGAGTGGTTCCAGAGGCTCAGAGCTGGCA
 CCCCTCAGTGCCCCGTTTGGAGAGTGAAGTGTATCACTGCGAGTGTGGGGTAAAGTGGGAGCAGAGGCTGTG
 GTGAGTGGGTGAGGAGCTGGTCTGGAGTAGGGAGACTTCGCGAGGAGGCTCTGGAAGAAGTGTCAAGGTCA
 CTGTGTCCAGTGCCTTCGGGGGCACTCAGTGTCTGCTCTGCTGTGTACAGGCGAGGGTGTGCTCAGTGTGAGC
 GGGATAGTGTCTCACTGCACTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 GCGCGCGTAAAGTGAAGGAGTCCAGGGTCAGCAGCTGTGATGTGAGGGCTCACTGCTGCTGGGACTCTGATCAG
 GGAAGGAGCACTCAGTGTGTGAGGAACAGTGCAGCTGCTCACAAGTGCATTCCAAATCACTTCAAGCA
 ACTGTGTGAATGTGTTATTATGACCTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAATTAAGCAACGAG
 ATGAAGTGCACCGAGCTGTGTGCACTGACCTGTTTGAAGAAATATGGCTTTCTGGGACAGGCGAGGATGCTT
 TGCCCTGCCCTCTATGCTCACTGTGCTCTCCACTCCCTCTCCCTCCTCCAACTTCCCTCCCTTCTGTCTCC
 AGCAGCCCGAGAGACCAAGCTGATCCAGAGCTGGAGAAAGAACCGAGAGGCTTCAGGAGGCGAGCAGAGGGG
 AAGTGACCAAGAGGAGCT
 CCAGTGCCTTTGTCTCTCTCTGCTGCTCTACTCCACCCCACTACCTTCGGAACTTCGGAACCAAGCTCCACGGGG
 GAGAGGCGAGTGGGCGAGGAGGTCAGAGCCACTCAAGTCTGCGCTGCCACCTTCGGGCTCTGTGCTGGAA
 GCGCCACCCCTTTCTCTGCTGCAATGATGTCACTGGCTTGTGGGATTTTAAATTTATCTCACTCAGCAGCAAG
 GCGCCCGGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCAATTAAGGAGGTTTGTATTATTAAGAA
 ATTTCTTTTTCAGTCTTTGGGCTAGGAGTGTGGCTCTTTTGGCGGAGGAACCTGAGTGGGGGCTGGTGGAGAGGG
 CGNGAGGATGGAGGTGAGAGAGGAGGAGCTGTGACACTTGGGGAGCTGAAAGAGACTGGAGAGGCGAGAGGATAG
 CTGTGCNNITAGCTGTCATNCTGCGTTCGCGAGAGGGCTGGGATGGTTGTGAGATGGTGTAGAGAGCTCAAG
 AATTTAGGGAAGTAGAGCAGGATTTTGAATCAAGTATTTAGTTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT
 TTTGAAGTTGCTCCAGAGGAGATCAAGGTGTACACAGCCGCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT

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[illegible]

GGCCGAGCGGGGGTGTCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCCGCGGCCCGGAGCGGGGCAGCTGCGGGGAGCCCTGAATACCGCCTTGGCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCAGCGACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGCTGGATTGGA
GGAACCCCTGCCCGATGGCGTTCTCGTGTGAACACCTTCAACAGCCTGTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGA AAAACA CACCTTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCGC
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTAC
CGTCTACATCAGTCCGACTCTAAGAGTTCCAAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCTGTGTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAAATGCCCCT
CCTTTCTTTCTTTCTTTCTTCTCCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCTC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG
GAGATATAAGTTTCCGAGCTTGCACAGGAAGCGTTCAAGTGTGAGTGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCTGAGGATTCCAGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAAAGAGATTGCATTGAGCCAGGTCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAACCTAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCC
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACCTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CTTGGTGGCAGAAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGGC
ACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT
GCCTCCAGCAGAGCCCCACCATTCAGTGTGACATCTTCCGTGTACCTGCCTGGAAGAG
GTCTGGTGGGGAGGCCAGTTCCCATAGGAAGGAGCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCTGGCGGCCATGGGGCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGTAAGTGGTTCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGTTGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

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FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCCGAGA
GGAGGGGAGGCAAAAACCCGAAAAACAAAAGAGAGAAACAACACCCAACTGGGGTGG
GGGGAGAAAGAAAAGAAAAGAAACCCACCACCACCAAAAAAATAAAAAAAAAAAAAA
AAAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCTCGGGAAGACTCGCCAGCACCCAGGGGG
TGGGGGAGTGCAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG
CTGTTGGTGACGGGTGCTTGTGTGCTCGAACCAGTGGCTGGCGGCGGTGCTCCTCAGCTGTG
CTGCTGTCTACCTCTCTGCTCCCGCTGGACAGAGTGTGGAATTCCTCCCTGGGCGGCGGTG
ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT
TCAAAGGGTGCTGGCTGAACCGGTCAAGTATTATTTTGGCGGAGGTGATAAGTGGTCAGT
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCTCCAGATACAGAATG
TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTCAGACTCAACATACACCCAGAACA
ATGCAAGGTGACATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAATATGATATGAC
CGTCAATGAAGGAACCAACGTCACCTTACTTGTGTCCTGGCCACTGGGAAACCCAGAGCCTTCCA
TTTCTTGGCGACACATCTCCCCATCAGCAAAACCAATTGAAAATGGACAATATTTGGACATT
TATGGAATTACAAGGACCAGGCTGGGGAATATGAATGCAAGTGGCGGAAAAATGCTGTGTCAAT
CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTACTTCAGGAAATTAAT
CTGGCACCCTGACCCCGGACGCAAGTGGCTGTATAAGATGTGAAGGTGCAAGTGTGCGCCCT
CCAGCCTTTGAATGGTACAAAGGAGAGAGAAGAAGCTCTCAATGGCCAACAGGAATATTAT
TCAAATTTTAGCACAGATCCATTCTCACTGTTACCAAGTGACACAGGAGCACTTCGGCA
ATTATACCTGTGTGGCTGCCAACAAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCT
CCAAGTACAGCCAGTATGGAATTACCGGAGCGCTGATGTTCTTTCTCTCTGCTGGTACCT
TGTGTGACACTGCTCTCTTCCACAGCATATCTACCTGAAGAATGCCATTCTACAAT~~TAAA~~
TTCAAAGACCCATAAAAGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT
GGTACAGTTTGTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
TTCTGTAGAATTGCTCATTATGTAATACTTTAATTCCTACTCTTTTGTATTAGCTACATTA
CCTTGTAAGCAGTACACATGTCTCTTTTAAAGAGCTGAAAGCTCTGAAATTACTTTTAG
AGGATATTAATTTGTGATTTTCAATGTTGTAATCTACAACCTTTCAAAGCATTCAGTCATGGT
CTGCTAGGTTGCAAGCTGTAGTTTACAAAACGAATATTGCAAGTGAATATGTGATTCTTTAA
GGCTGCAATACAAGCATTCAGTTCCCTGTGTTCAATAAGAGTCAATCCACATTTACAAGATG
CATTTTTTTCTTTTGTATAAAAAAGCAAAATAATATGCTTCAGATTAATTTCTTCAAATA
TAACACATATCTAGATTTTCTGCTTGATGATTAATTCAGGATTCAGGATGAGCCTGTGTAAT
ATAACTGGCTGTGCAAGCTCTGCTTCTCTTTCGTGAAGTTCAGCATGGGTGTCCTTATAC
AATAATATTTTCTCTTTGTCTCCAACTAATATAAATGTTTTGCTAAATCTTACAATTTGA
AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTAAGTAAACGAAGGAGC
TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCACT
AACTCAGTTCTTGTGATGAGAGCAATTAATAACAGTATAGTAATATACCATATGATTTCT
TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCTTAAATGACAGACA
GTCCACTCAAAGGATGCTCAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAAA
TTTTAAGATGATTTGTGCAAAAGGCGACAAGTCCTTCACTAATATTACAAGATTGGTA
AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA
TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCCAGGTGGTTATGACCCGCTACTC
AGGAGGAAATTACAGAGACAATTATGACAACTGAAATGAGACATGCAATATATAGATACA
CAAGGAATAATTTCTGATCAGGATCGTCTTCCAATGGCTGTATTATAAGGTTTTTGG
AGCTCAGCTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTAAATTTGACCTGCCA
AGGTAGCTGAAGACCTTTTAGACAGTTCATCTTTTTTTTAAATTTTCTGCTTATTTAA
AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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 92. *Table of Operators*
 93. *Table of Symbols*
 94. *Table of Abbreviations*
 95. *Table of Acronyms*
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 97. *Table of Conversions*
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 144. *Table of Abbreviations*
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 185. *Table of Acronyms*
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 203. *Table of Symbols*
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 214. *Table of Abbreviations*
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 217. *Table of Conversions*
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 221. *Table of Functions*
 222. *Table of Operators*
 223. *Table of Symbols*
 224. *Table of Abbreviations*
 225. *Table of Acronyms*
 226. *Table of Units*
 227. *Table of Conversions*
 228. *Table of Constants*

Important features of the protein:

amino acids 1-31

amino acids 326-345

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

amino acids 147-151, 208-212, 224-228

amino acids 178-186

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACACCAATTGCAATGGAGCCTTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTACCCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTTGAGATGTATTCTCTCAATGACACTCTGGCGGTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCTTCGAGGCCAACTCACCTGGGTCCGCTCAGCCATGAGCACTTGCTGCAGCGGT
AGACAACCTTCACTCAGAACCCAGGGATGTTTCAAGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCAACAAGGGGCCATGGGCATGCCTGGTGCCTTGGCCCGCCGGGACCACCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCCAAAAGGGGAACTGGAACTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGGGGCTCCTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTTCTCTGGAGCTAAAGGAGAT
CAAGGACAACCTGGAGTGCAGGGTGTTCGGGGCCTCCTGGTGCAGTGGGACACCCAGGTGC
CAAGGTGAGCCTGGCAGTGTGGTCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAGAGAGTGAAAACTCAGTGTC
GTCAGGATTGTGGCAGTAGTAACCGAGGCCGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCACTGTGCGGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGCGAGCGTGGAGTGCAGCGCTGGAACCCGAAAACCCCTTCA
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAFAHQIAMEPFPEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGSPGPQGPVGVKGEAGLQGPQGAAPGKQGATGTPGPQGEKSGKGDGGLIGPKGETGTKGE
KGDLLGLPGSKGDRGMKGDAVVMGPPGAQGSKGDGFRPGPPGLAGFPKAKGDQGGPGLQGVPG
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKSGKDTGLQGGQGRKGESGVPGPA
GVKGEQGSPLAGPKGAPGQAGKGDQGVKGSSEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWTGTICDDEWQNSDAIVFCRMLGYSGRALYKVGAGTGQIWLDDNVQCRGTESTLW
SCTKNSWGHHDCHSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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CCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAATGAAACTGATGGTACTTGTTTTCAC
CATTGGGCTAACTTTGTGTCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACTGTACAACTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCAAAAGACGTTTTCTTTGGACCAAAGATCTCTTCG
TGATTCCTTGCAACAATCAATGGAATCTTCATGTATTCTGGAGAACACCATTCCTGATTTTC
CCACAAACTCTACTACATCAGTATAAATGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATCTTACTTGTCTTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAACTCAAAAAA

FIGURE 234

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758
<subunit 1 of 1, 98 aa, 1 stop
<MW: 11081, pI: 6.68, NX(S/T): 1
MKLMVLVFTIGLTLLLG VQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ
```

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71



FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLHETDSAVATARRPRWLCAGALVLGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFLL
DELKAENIKKFLHNFTQIPHLAGTEQNFLAKQIQSQWKEFGLDVELAHYDVLLSYPNKTH
PNYISIIINEDGNEIFNTSLFEPPPPGYENVSDIVPPPSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVARIYRGKVFRGNKVKNQLAGAKGVILYSDPADYFAPGVKSYPDGWNLL
PGGGVQVRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDYRV
ILGGHRDSWVFGGIDPQSGAAVVEIIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYES
WTKKSPSPSEFGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWTNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCCRDAYVVLRYADKIYSISMKHPQ
EMKTYSVSPDSLFSAVKNFTETASKFSERLQDFDKSNPIVLRMMNDQLMFLEAFIDPLGLP
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713